



SUBSTITUTE SEQUENCE LISTING

<110> Sleeman, Matthew
Murison, Greg

<120> Fibroblast Growth Factor Receptors and Methods for Their Use

<130> 11000.1037c5

<150> U.S. 09/823,038

<151> 2001-03-28

<150> U.S. 09/383,586

<151> 1999-08-26

<150> U.S. 09/276,268

<151> 1999-03-25

<150> PCT/NZ00/00015

<151> 2000-02-18

<150> U.S. 60/221,216

<151> 2000-07-25

<150> U.S. 10/157,444

<151> 2000-05-28

<150> PCT/NZ03/00105

<151> 2003-05-27

<160> 145

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 384

<212> DNA

<213> Mouse

<220>

<221> misc_feature

<222> (1)...(384)

<223> n = A,T,C or G

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tgtgggtggc	cagaagtttg	tgggtgtgcc	cacgggtgat	gtgtgggtcac	ggcctgatgg	180
ctcctacctc	aacaagctgc	tcatctctcg	ggcccggcag	gatgatgctg	gcatgtacat	240
ctgcctaggt	gcaaatacca	tgggctacag	tttccgtagc	gccttcctca	ctgtattacc	300
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<211> 1967

<212> DNA

<213> Mouse

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caaacttggc	catatagatg	tatgtactac	cagatgaaca	gccagccaga	ttcacacacg	1860
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cgcccccgcg	ctgatccctg	tcgagcgtct	acgcgcctcg	cttcctttgc	ctggagctcg	300
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gtgccagtgg	agggggaccc	gccgccgctg	accatgtgga	ccaaggatgg	ccgcaccatc	240
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cgccacaact	ccaccatcga	tgtgggcggc	cagaagtttg	tggtgctgcc	cacgggtgac	960
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<220>
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Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile
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Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu
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Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser
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Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
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Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
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Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
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Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
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Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys
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Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu
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Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro
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<400> 7															
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Ala	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	
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Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	
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Asp	Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	
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	370					375					380					
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385					390					395					400	
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<400> 8																
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Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	
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Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	
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Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	
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His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu	Thr	
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Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	
	195					200					205					
Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	
	210					215					220					
Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	
225					230				235						240	
Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	
				245					250					255		
Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	
		260					265						270			
Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ala	
	275					280					285					
Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	
	290					295				300						
Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	
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Asn	Lys	Pro	Leu													

<210> 9
 <211> 1423
 <212> DNA
 <213> Mouse

<400> 9
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 gccggtgcc tcaacgccac ctacaaagtg gatgtaatcc gtgagtgggt ggtctgtggt 240
 aggacagggg cccgtgggtgc ctaaaactgt gctgacatgt ttgtttttcc ttggcttaga 300
 gcggactcgt tccaagcctg tgctcacagg gacacaccct gtgaacacaa cgggtggactt 360
 cgggtgggaca acgtccttcc agtgcaaggt gcgcagtgc gtgaagcctg tgatccagtg 420
 gctgaagcgg gtggagtacg gctccgaggg acgccacaac tccaccattg atgtgggtg 480
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<210> 10
 <211> 35
 <212> DNA
 <213> Mouse

<400> 10
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<210> 11
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<400> 11
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<210> 12
 <211> 18
 <212> DNA
 <213> Mouse

<400> 12
 ctgtgcggct caagtgtg 18

<210> 13
 <211> 373
 <212> PRT
 <213> Mouse

<400> 13
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 20 25 30
 Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
 35 40 45
 Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
 50 55 60
 Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
 65 70 75 80
 Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
 85 90 95
 Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
 100 105 110
 Met Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly Pro Gly Gly Ser
 115 120 125
 Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp Ala Arg Pro Arg
 130 135 140
 Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val
 145 150 155 160
 Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro
 165 170 175
 Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu Thr His Leu Glu Ala
 180 185 190
 Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys

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Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg			
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Pro Asp Gly Ser Tyr			
35			

<210> 16
 <211> 1515
 <212> DNA
 <213> Human

<400> 16

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gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggatgacatt	360
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agccagcagt	gggcacgacc	gcgcttcaca	cagccctcca	agatgaggcg	ccgggtgatc	480
gcacggcccc	tgggtagctc	cgtgcggctc	aagtgcgtgg	ccagcgggca	ccctcggccc	540
gacatcacgt	ggatgaagga	cgaccaggcc	ttgacgcgcc	cagaggccgc	tgagcccagg	600
aagaagaagt	ggacactgag	cctgaagaac	ctgcgggccg	aggacagcgg	caaatacacc	660
tgccgcgtgt	cgaaccgcgc	gggcgccatc	aacgccacct	acaagggtga	tgtgatccag	720
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<210> 17
 <211> 504
 <212> PRT
 <213> Human

<400> 17

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	20
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg	
	35
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr	
	50
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu	
65	70
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val	
	85
	90
	95

<400> 18

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gcccggctgg gccgcactgt gcggctgcag tgcccagtgg agggggaccc gccgcccgtg    180
accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg    240
ccgcaggggc tgaaggtgaa gcaggtggag cgggaggatg ccggcgtgta cgtgtgcaag    300
gccaccaacg gcttcggcag ccttagcgtc aactacaccc tcgtcgtgct ggatgacatt    360
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gcacggcccg tgggtagctc cgtgcggctc aagtgcgtgg ccagcgggca ccctcggccc    540
gacatcacgt ggatgaagga cgaccaggcc ttgacgcgcc cagaggccgc tgagcccagg    600
aagaagaagt ggacactgag cctgaagaac ctgcggccgg aggacagcgg caaatacacc    660
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<210> 19

<211> 386

<212> PRT

<213> Human

<400> 19

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Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
                20                25                30
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
    35              40              45
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
    50              55              60
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
    65              70              75              80
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
                85              90              95
Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
    100            105            110
Thr Leu Val Val Leu Asp Asp Ile Ser Pro Gly Lys Glu Ser Leu Gly
    115            120            125
Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp
    130            135            140
Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val Ile

145              150              155              160
Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly
                165              170              175
His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp Asp Gln Ala Leu Thr

                180              185              190
Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu
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<213> Human

<400> 21

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			20					25					30		
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
		35				40						45			
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr
	50					55					60				
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
65					70					75					80
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
				85					90					95	
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
			100					105					110		
Thr	Leu	Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly
		115				120						125			
Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp
	130					135					140				
Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn
145					150					155					160
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg
			165						170					175	
Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly
			180					185					190		
Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe
		195					200					205			
Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr
	210					215					220				
Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met
225					230					235					240
Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala
			245						250					255	
Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Gln	Gly	Pro	Pro	Val	Ala
			260					265					270		
Ser	Ser	Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile
		275					280					285			
Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys
	290					295				300					
Gln	Ala	Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro
305					310					315					320
Gly	His	Arg	Pro	Pro	Gly	Thr	Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp
			325						330					335	
Leu	Pro	Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys
			340					345					350		
Glu	Glu	His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly
		355					360					365			
Pro	Val	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His
	370					375					380				
Thr	His	Thr	His	Thr	His	Ser	His	Thr	His	Ser	His	Val	Glu	Gly	Lys
385					390					395					400
Val	His	Gln	His	Ile	His	Tyr	Gln	Cys							
				405											

<210> 22

<211> 1434
 <212> DNA
 <213> Human

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 accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg 240
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<210> 23
 <211> 477
 <212> PRT
 <213> Human

<400> 23
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 35 40 45
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
 50 55 60
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
 65 70 75 80
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
 85 90 95
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100 105 110
 Thr Leu Val Val Leu Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met
 115 120 125
 Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys
 130 135 140
 Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp
 145 150 155 160
 Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys

				165				170						175			
Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr		
			180					185					190				
Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys		
		195					200					205					
Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr		
	210					215					220						
His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln		
225					230				235						240		
Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg		
			245					250					255				
Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly		
			260				265						270				
Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro		
	275					280					285						
Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp		
	290				295						300						
Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser		
305					310				315						320		
Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Gln	Gly		
			325					330						335			
Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro	Val		
		340						345					350				
Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	Leu		
	355					360						365					
Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	Ala		
	370					375					380						
Pro	Pro	Leu	Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ala	Arg	Asp	Arg	Ser		
385					390				395						400		
Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly		
			405					410					415				
Val	Gly	Leu	Cys	Glu	Glu	His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu		
		420					425					430					
Leu	Gly	Pro	Gly	Pro	Val	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr		
	435					440					445						
Thr	Asp	Ile	His	Thr	His	Thr	His	Thr	His	Ser	His	Thr	His	Ser	His		
	450				455						460						
Val	Glu	Gly	Lys	Val	His	Gln	His	Ile	His	Tyr	Gln	Cys					
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<210> 24
 <211> 1242
 <212> DNA
 <213> Human

<400> 24

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caccccgtga	acacgacggt	ggacttcggg	gggaccacgt	ccttccagtg	caaggtgcgc	540
agcgacgtga	agccggtgat	ccagtggctg	aagcgcgtgg	agtacggcgc	cgagggccgc	600
cacaactcca	ccatcgatgt	gggcggccag	aagtttgtgg	tgctgcccac	gggtgacgtg	660

tggtcgcggc	ccgacggctc	ctacctcaat	aagctgctca	tcacccgtgc	ccgccaggac	720
gatgcgggca	tgtacatctg	ccttggcgcc	aacaccatgg	gctacagctt	ccgcagcgcc	780
ttcctcaccg	tgctgccaga	cccaaaaccg	caagggccac	ctgtggcctc	ctcgtcctcg	840
gccactagcc	tgccgtggcc	cgtgggtcatc	ggcatcccag	ccggcgctgt	cttcatacctg	900
ggcacccctgc	tcctgtgggt	ttgccaggcc	cagaagaagc	cgtgcacccc	cgcgccctgcc	960
cctcccctgc	ctgggcaccg	cccgccgggg	acggcccgcg	accgcagcgg	agacaaggac	1020
cttccctcgt	tggccgccct	cagcgctggc	cctgggtgtgg	ggctgtgtga	ggagcatggg	1080
tctccggcag	ccccccagca	cttactgggc	ccaggcccag	ttgctggccc	taagttgtac	1140
cccaaactct	acacagacat	ccacacacac	acacacacac	actctcacac	acactcacac	1200
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<210> 25

<211> 413

<212> PRT

<213> Human

<400> 25

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
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Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly
			20					25					30		
Lys	Glu	Ser	Leu	Gly	Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro
		35				40						45			
Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met
	50					55					60				
Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys
65					70				75						80
Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp
				85					90					95	
Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys
			100					105					110		
Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr
		115					120					125			
Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys
	130					135					140				
Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr
145					150					155					160
His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln
				165					170					175	
Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg
		180					185						190		
Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly
	195						200					205			
Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro
	210					215					220				
Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp
225					230					235					240
Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser
				245					250					255	
Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Gln	Gly
			260					265						270	
Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro	Val
		275					280					285			
Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	Leu
	290					295					300				
Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	Ala
305				310						315					320

Pro	Pro	Leu	Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ala	Arg	Asp	Arg	Ser
				325					330					335	
Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly
			340					345					350		
Val	Gly	Leu	Cys	Glu	Glu	His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu
		355					360					365			
Leu	Gly	Pro	Gly	Pro	Val	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr
	370					375					380				
Thr	Asp	Ile	His	Thr	His	Thr	His	Thr	His	Ser	His	Thr	His	Ser	His
385					390					395					400
Val	Glu	Gly	Lys	Val	His	Gln	His	Ile	His	Tyr	Gln	Cys			
			405					410							

<210> 26
 <211> 876
 <212> DNA
 <213> Human

<400> 26

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gcccggctgg	gccgcactgt	gcggtctgcag	tgcccagtgg	agggggaccc	gccgccgctg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggatgacatt	360
agcccagggg	aggagagcct	ggggccccgac	agctcctctg	ggggtcaaga	ggaccccgcc	420
agccagcagt	gggacccaaa	accgcaaggg	ccacctgtgg	cctcctcgtc	ctcggccact	480
agcctgccgt	ggcccgtggg	catcggcatc	ccagccggcg	ctgtcttcat	cctgggcacc	540
ctgctcctgt	ggctttgcca	ggcccagaag	aagccgtgca	cccccgcgcc	tgcccctccc	600
ctgcctgggc	accgcccgcc	ggggacggcc	cgcgaccgca	gcggagacaa	ggaccttccc	660
tcgttggccg	ccctcagcgc	tggccctggg	gtggggctgt	gtgaggagca	tgggtctccg	720
gcagcccccc	agcacttact	gggcccaggc	ccagttgctg	gccctaagtt	gtaccccaaa	780
ctctacacag	acatccacac	acacacacac	acacactctc	acacacactc	acacgtggag	840
ggcaaggtcc	accagcacat	ccactatcag	tgctag			876

<210> 27
 <211> 291
 <212> PRT
 <213> Human

<400> 27

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
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Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala
			20				25						30		
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
		35				40						45			
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr
	50					55					60				
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
65					70					75					80
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
				85				90					95		
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
			100				105						110		
Thr	Leu	Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly
			115				120					125			

Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp
130						135					140				
Asp	Pro	Lys	Pro	Gln	Gly	Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr
145					150					155					160
Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe
				165					170					175	
Ile	Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro
			180					185					190		
Cys	Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly	His	Arg	Pro	Pro	Gly
		195					200					205			
Thr	Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Ala
		210				215					220				
Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu	Glu	His	Gly	Ser	Pro
225					230					235					240
Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro	Val	Ala	Gly	Pro	Lys
				245					250					255	
Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr	His	Thr	His	Thr	His
			260					265					270		
Ser	His	Thr	His	Ser	His	Val	Glu	Gly	Lys	Val	His	Gln	His	Ile	His
		275					280					285			
Tyr	Gln	Cys													
		290													

<210> 28
 <211> 1080
 <212> DNA
 <213> Human

<400> 28

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gcccggctgg	gccgcactgt	gcggtctgcag	tgcccagtgg	agggggagccc	gccgccgctg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcagggggc	tgaagggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggcacgaccg	360
cgtttcacac	agccctccaa	gatgaggcgc	cgggtgatcg	cacggcccgt	gggtagctcc	420
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gaccaggcct	tgacgcgccc	agaggccgct	gagcccagga	agaagaagtg	gacactgagc	540
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ggcgccatca	acgccaccta	caaggtggat	gtgatccacc	caaaaccgca	agggccacct	660
gtggcctcct	cgctcctcgg	cactagcctg	ccgtggcccc	tggtcatcgg	catcccagcc	720
ggcgctgtct	tcctcctggg	caccctgctc	ctgtggcttt	gccaggccca	gaagaagccg	780
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cgcagcggag	acaaggacct	tccctcgttg	gccgccctca	gcgtggccc	tggtgtgggg	900
ctgtgtgagg	agcatgggtc	tccggcagcc	ccccagcact	tactggggccc	aggcccagtt	960
gctggcccta	agttgtaccc	caaactctac	acagacatcc	acacacacac	acacacacac	1020
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<210> 29
 <211> 359
 <212> PRT
 <213> Human

<400> 29

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Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met
														Ala

			20					25					30				
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg		
		35					40					45					
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr		
	50					55					60						
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu		
65					70					75					80		
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val		
			85					90					95				
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr		
			100					105					110				
Thr	Leu	Val	Val	Leu	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met		
		115					120					125					
Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys		
	130					135					140						
Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp		
145					150					155					160		
Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys		
			165					170					175				
Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr		
		180						185					190				
Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys		
		195					200					205					
Val	Asp	Val	Ile	His	Pro	Lys	Pro	Gln	Gly	Pro	Pro	Val	Ala	Ser	Ser		
	210					215					220						
Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala		
225					230					235					240		
Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln	Ala		
			245					250						255			
Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly	His		
			260					265					270				
Arg	Pro	Pro	Gly	Thr	Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro		
		275					280					285					
Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu	Glu		
	290					295					300						
His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro	Val		
305					310					315					320		
Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr	His		
			325					330					335				
Thr	His	Thr	His	Ser	His	Thr	His	Ser	His	Val	Glu	Gly	Lys	Val	His		
			340					345					350				
Gln	His	Ile	His	Tyr	Gln	Cys											
		355															

<210> 30

<211> 1149

<212> DNA

<213> Human

<400> 30

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gcccggtctg	gccgcactgt	gcggctgcag	tgcccagtg	agggggaccc	gccgccgctg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggagcggacc	360
cgttccaagc	ccgtgctcac	aggcacgcac	cccgtgaaca	cgacgggtgga	cttcgggggg	420

accacgtcct	tccagtgcaa	ggtgcgcagc	gacgtgaagc	cggatgatcca	gtgggtgaag	480
cgcgtggagt	acggcgccga	gggccgccac	aactccacca	tcgatgtggg	cggccagaag	540
tttgtggtgc	tgcccacggg	tgacgtgtgg	tcgcggcccg	acggctccta	cctcaataag	600
ctgctcatca	cccgtgcccc	ccaggacgat	gcgggcatgt	acatctgcct	tggcgccaac	660
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aagaagccgt	gcacccccgc	gcctgcccct	cccctgcctg	ggcaccgccc	gccggggacg	900
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ggcccagttg	ctggccctaa	gttgtacccc	aaactctaca	cagacatcca	cacacacaca	1080
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cagtgtctag						1149

<210> 31
 <211> 382
 <212> PRT
 <213> Human

<400> 31

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Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala
			20					25					30		
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
		35					40					45			
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr
	50					55					60				
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
65					70				75					80	
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
				85					90					95	
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
			100					105					110		
Thr	Leu	Val	Val	Leu	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly
		115					120					125			
Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe
	130					135					140				
Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys
145				150					155					160	
Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val
			165					170						175	
Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg
		180					185					190			
Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln
	195					200						205			
Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr
	210				215						220				
Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Gln
225				230						235					240
Gly	Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro
			245					250						255	
Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu
		260					265					270			
Leu	Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro
	275					280						285			

Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys
130						135					140				
Val	Asp	Val	Ile	His	Pro	Lys	Pro	Gln	Gly	Pro	Pro	Val	Ala	Ser	Ser
145					150					155					160
Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala
				165					170					175	
Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln	Ala
			180					185					190		
Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly	His
		195					200					205			
Arg	Pro	Pro	Gly	Thr	Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro
	210					215					220				
Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu	Glu
225					230					235					240
His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro	Val
				245					250					255	
Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr	His
			260					265					270		
Thr	His	Thr	His	Ser	His	Thr	His	Ser	His	Val	Glu	Gly	Lys	Val	His
		275					280					285			
Gln	His	Ile	His	Tyr	Gln	Cys									
	290					295									

<210> 34
 <211> 957
 <212> DNA
 <213> Human

<400> 34

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tcctctgggg	gtcaagagga	ccccgccagc	cagcagtggg	agcggacccg	ttccaagccc	180
gtgctcacag	gcacgcaccc	cgtgaacacg	acggtggact	tcggggggac	cacgtccttc	240
cagtgcgaagg	tgcgcagcga	cgtgaagccg	gtgatccagt	ggctgaagcg	cgtggagtag	300
ggcgccgagg	gccgccacaa	ctccaccatc	gatgtgggcg	gccagaagtt	tgtggtgctg	360
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cgtgcccgcc	aggacgatgc	gggcatgtac	atctgccttg	gcgccaacac	catgggctac	480
agcttccgca	gcgccttcct	caccgtgctg	ccagacccaa	aaccgcaagg	gccacctgtg	540
gcctcctcgt	cctcggccac	tagcctgccg	tggcccgtgg	tcatcggcac	cccagccggc	600
gctgtcttca	tcctgggcac	cctgctcctg	tggctttgcc	aggcccagaa	gaagccgtgc	660
acccccgcgc	ctgccccctc	cctgcctggg	caccgccccg	cggggacggc	ccgcgaccgc	720
agcggagaca	aggaccttcc	ctcgttggcc	gccctcagcg	ctggccctgg	tgtggggctg	780
tgtgaggagc	atgggtctcc	ggcagcccc	cagcacttac	tgggcccagg	cccagttgct	840
ggccctaagt	tgtaccccaa	actctacaca	gacatccaca	cacacacaca	cacacactct	900
cacacacact	cacacgtgga	gggcaaggtc	caccagcaca	tccactatca	gtgctag	957

<210> 35
 <211> 318
 <212> PRT
 <213> Human

<400> 35

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10					15	
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly
			20					25					30		
Lys	Glu	Ser	Leu	Gly	Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro

ccgccgggga	cggccccgcga	ccgcagcggga	gacaaggacc	ttccctcgtt	ggccgcctc	960
agcgctggcc	ctggtgtggg	gctgtgtgag	gagcatgggt	ctccggcagc	ccccagcac	1020
ttactggggc	caggcccagt	tgctggccct	aagttgtacc	ccaaactcta	cacagacatc	1080
cacacacaca	cacacacaca	ctctcacaca	cactcacacg	tggagggcaa	ggtcaccag	1140
cacatccact	atcagtgcta	g				1161

<210> 37
 <211> 386
 <212> PRT
 <213> Human

<400> 37

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10					15	
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Ala	Arg	Pro	Arg	Phe	Thr
			20					25					30		
Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser
		35					40					45			
Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile
	50					55					60				
Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu
65				70						75					80
Pro	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu
			85						90					95	
Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile
			100					105					110		
Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro
		115					120					125			
Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly
	130					135					140				
Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile
145				150						155					160
Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser
			165						170					175	
Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp
		180						185					190		
Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr
		195				200						205			
Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn
	210					215					220				
Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp
225				230						235					240
Pro	Lys	Pro	Gln	Gly	Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser
			245						250					255	
Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile
		260					265						270		
Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro	Cys
	275						280					285			
Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly	His	Arg	Pro	Pro	Gly	Thr
	290					295					300				
Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Ala	Leu
305					310				315						320
Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu	Glu	His	Gly	Ser	Pro	Ala
			325						330					335	
Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro	Val	Ala	Gly	Pro	Lys	Leu
		340					345						350		
Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr	His	Thr	His	Thr	His	Ser

	355		360		365
His Thr	His Ser His Val	Glu Gly Lys Val	His Gln	His Ile His Tyr	
370		375		380	
Gln Cys					
385					

<210> 38
 <211> 795
 <212> DNA
 <213> Human

<400> 38

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gcccggctgg	gccgcactgt	gcggctgcag	tgcccagtgg	agggggaccc	gccgccgctg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaaggatga	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggacccaaaa	360
ccgcaagggc	cacctgtggc	ctcctcgtcc	tcggccacta	gcctgccgtg	gcccgtggtc	420
atcggcatcc	cagccggcgc	tgtcttcac	ctgggcaccc	tgctcctgtg	gctttgccag	480
gcccagaaga	agccgtgcac	ccccgcgcct	gcccctcccc	tgctggggca	ccgcccgccg	540
gggacggccc	gcgaccgcag	cggagacaag	gaccttcctt	cgttgggccg	cctcagcgct	600
ggccctggtg	tggggctgtg	tgaggagcat	gggtctccgg	cagcccccca	gcacttactg	660
ggcccaggcc	cagttgctgg	ccctaagttg	taccccaaac	tctacacaga	catccacaca	720
cacacacaca	cacactctca	cacacactca	cacgtggagg	gcaagggtcca	ccagcacatc	780
cactatcagt	gctag					795

<210> 39
 <211> 264
 <212> PRT
 <213> Human

<400> 39

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu	
1 5 10 15	
Gly Ala Phe Pro Pro Ala Ala Ala Arg Gly Pro Pro Lys Met Ala	
20 25 30	
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg	
35 40 45	
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr	
50 55 60	
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu	
65 70 75 80	
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val	
85 90 95	
Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr	
100 105 110	
Thr Leu Val Val Leu Asp Pro Lys Pro Gln Gly Pro Pro Val Ala Ser	
115 120 125	
Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro	
130 135 140	
Ala Gly Ala Val Phe Ile Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln	
145 150 155 160	
Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly	
165 170 175	
His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu	
180 185 190	

Pro	Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu
		195					200					205			
Glu	His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro
	210					215					220				
Val	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr
225					230					235					240
His	Thr	His	Thr	His	Ser	His	Thr	His	Ser	His	Val	Glu	Gly	Lys	Val
				245					250					255	
His	Gln	His	Ile	His	Tyr	Gln	Cys								
			260												

<210> 40
 <211> 603
 <212> DNA
 <213> Human

<400> 40

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tcctctgggg	gtcaagagga	ccccgccagc	cagcagtggg	acccaaaacc	gcaagggcca	180
cctgtggcct	cctcgtcctc	ggccactagc	ctgccgtggc	ccgtgggtcat	cggcatccca	240
gccggcgctg	tcttcattct	gggcaccctg	ctcctgtggc	tttgccaggc	ccagaagaag	300
ccgtgcaccc	ccgcgcctgc	ccctcccctg	cctggggcacc	gcccgcgggg	gacggcccgc	360
gaccgcagcg	gagacaagga	ccttcctctg	ttggccgccc	tcagcgctgg	ccctgggtgtg	420
gggctgtgtg	aggagcatgg	gtctccggca	gccccccagc	acttactggg	cccaggccca	480
gttgctggcc	ctaagttgta	ccccaaactc	tacacagaca	tccacacaca	cacacacaca	540
cactctcaca	cacactcaca	cgtggagggc	aaggtccacc	agcacatcca	ctatcagtgc	600
tag						603

<210> 41
 <211> 200
 <212> PRT
 <213> Human

<400> 41

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10				15		
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly
			20					25					30		
Lys	Glu	Ser	Leu	Gly	Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro
		35					40					45			
Ala	Ser	Gln	Gln	Trp	Asp	Pro	Lys	Pro	Gln	Gly	Pro	Pro	Val	Ala	Ser
	50					55					60				
Ser	Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro
65					70					75					80
Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln
				85					90					95	
Ala	Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly
			100					105					110		
His	Arg	Pro	Pro	Gly	Thr	Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	Leu
	115						120					125			
Pro	Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu
	130					135					140				
Glu	His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro
145					150					155					160
Val	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr
				165					170					175	

His Thr His Thr His Ser His Thr His Ser His Val Glu Gly Lys Val
180 185 190
His Gln His Ile His Tyr Gln Cys
195 200

<210> 42
<211> 807
<212> DNA
<213> Human

<400> 42
atgacgccga gccccctgtt gctgctcctg ctgccgccgc tgctgctggg ggccttccca 60
ccggccgccg ccgcccagac acgaccgcgc ttcacacagc cctccaagat gaggcgccgg 120
gtgatcgcac ggcccgtggg tagctccgtg cggctcaagt gcgtggccag cgggcaccct 180
cggcccgcaca tcacgtggat gaaggacgac caggccttga cgcgcccaga ggccgctgag 240
cccaggaaga agaagtggac actgagcctg aagaacctgc ggccggagga cagcggcaaa 300
tacacctgcc gcgtgtcgaa ccgcgcgggc gccatcaacg ccacctacaa ggtggatgtg 360
atccacccaa aaccgcaagg gccacctgtg gcctcctcgt cctcggccac tagcctgccg 420
tgggcccggtg tcatcggcac cccagccggc gctgtcttca tcctgggcac cctgctcctg 480
tggttttgcc aggcccagaa gaagccgtgc acccccgcgc ctgcccctcc cctgcctggg 540
caccgcccgc cggggacggc ccgcgaccgc agcggagaca aggaccttcc ctcgttggcc 600
gccctcagcg ctggccctgg tgtggggctg tgtgaggagc atgggtctcc ggcagccccc 660
cagcacttac tgggcccagg cccagttgct ggccctaagt tgtaccccaa actctacaca 720
gacatccaca cacacacaca cacacactct cacacacact cacacgtgga gggcaaggtc 780
caccagcaca tccactatca gtgctag 807

<210> 43
<211> 268
<212> PRT
<213> Human

<400> 43
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
1 5 10 15
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Ala Arg Pro Arg Phe Thr
20 25 30
Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser
35 40 45
Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile
50 55 60
Thr Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu
65 70 75 80
Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu
85 90 95
Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile
100 105 110
Asn Ala Thr Tyr Lys Val Asp Val Ile His Pro Lys Pro Gln Gly Pro
115 120 125
Pro Val Ala Ser Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro Val Val
130 135 140
Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Leu Leu Leu
145 150 155 160
Trp Leu Cys Gln Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala Pro
165 170 175
Pro Leu Pro Gly His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser Gly
180 185 190

Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly	Val
		195					200					205			
Gly	Leu	Cys	Glu	Glu	His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu	Leu
	210					215					220				
Gly	Pro	Gly	Pro	Val	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr
225					230					235					240
Asp	Ile	His	Thr	His	Thr	His	Thr	His	Ser	His	Thr	His	Ser	His	Val
				245					250					255	
Glu	Gly	Lys	Val	His	Gln	His	Ile	His	Tyr	Gln	Cys				
			260					265							

<210> 44
 <211> 876
 <212> DNA
 <213> Human

<400> 44

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ccggccgccg	ccgccccgaga	gcggaccctg	tccaagcccg	tgctcacagg	cacgcacccc	120
gtgaacacga	cggtggactt	cggggggacc	acgtccttcc	agtgcaaggt	gcgcagcgac	180
gtgaagccgg	tgatccagtg	gctgaagcgc	gtggagtacg	gcgccgaggg	ccgccacaac	240
tccaccatcg	atgtgggcgg	ccagaagttt	gtggtgctgc	ccacgggtga	cgtgtggtcg	300
cggccccgacg	gctcctacct	caataagctg	ctcatcaccc	gtgcccgcga	ggacgatgcg	360
ggcatgtaca	tctgccttgg	cgccaacacc	atgggctaca	gcttccgcag	cgccttcctc	420
accgtgctgc	cagacccaaa	accgcaaggg	ccacctgtgg	cctcctcgtc	ctcggccact	480
agcctgccgt	ggcccgtggt	catcggcac	ccagccggcg	ctgtcttcat	cctgggcacc	540
ctgctcctgt	ggctttgcca	ggcccagaag	aagccgtgca	ccccgcgcc	tgcccctccc	600
ctgcctgggc	accgcccgcc	ggggacggcc	cgcgaccgca	gcggagacaa	ggaccttccc	660
tcgttggccg	ccctcagcgc	tggccctggt	gtggggctgt	gtgaggagca	tgggtctccg	720
gcagcccccc	agcacttact	gggcccaggc	ccagttgctg	gccctaagtt	gtaccccaaa	780
ctctacacag	acatccacac	acacacacac	acacactctc	acacacactc	acacgtggag	840
ggcaagggtcc	accagcacat	ccactatcag	tgctag			876

<210> 45
 <211> 291
 <212> PRT

<213> Human

<400> 45

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5				10					15		
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Glu	Arg	Thr	Arg	Ser	Lys
			20					25					30		
Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly
		35				40						45			
Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val
50					55						60				
Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn
65				70					75					80	
Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly
			85					90					95		
Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile
			100				105						110		
Thr	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala
		115					120					125			
Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro

130	135	140
Asp Pro Lys Pro Gln Gly	Pro Pro Val Ala Ser	Ser Ser Ser Ala Thr
145	150	155
Ser Leu Pro Trp Pro Val Val Ile Gly Ile	Pro Ala Gly Ala Val Phe	
165	170	175
Ile Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln Ala Gln Lys Lys Pro		
180	185	190
Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly His Arg Pro Pro Gly		
195	200	205
Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Ala		
210	215	220
Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu Glu His Gly Ser Pro		
225	230	235
Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro Val Ala Gly Pro Lys		
245	250	255
Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr His Thr His Thr His		
260	265	270
Ser His Thr His Ser His Val Glu Gly Lys Val His Gln His Ile His		
275	280	285
Tyr Gln Cys		
290		

<210> 46
 <211> 522
 <212> DNA
 <213> Human

<400> 46	
atgacgccga gccccctggt gctgctcctg ctgccgccgc tgctgctggg ggccttccca	60
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gccactagcc tgccgtggcc cgtgggtcatc ggcattcccag ccggcgctgt cttcatcctg	180
ggcaccctgc tcctgtggct ttgccaggcc cagaagaagc cgtgcacccc cgcgccctgcc	240
cctccccctgc ctgggcaccg cccgccgggg acggcccgcg accgcagcgg agacaaggac	300
cttccctcgt tggccgccct cagcgtctggc cctgggtgtgg ggctgtgtga ggagcatggg	360
tctccggcag cccccagca cttactgggc ccaggcccag ttgctggccc taagttgtac	420
cccaaactct acacagacat ccacacacac acacacacac actctcacac acactcacac	480
gtggagggca aggtccacca gcacatccac tatcagtgt ag	522

<210> 47
 <211> 173
 <212> PRT
 <213> Human

<400> 47
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
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Gly Ala Phe Pro Pro Ala Ala Ala Arg Asp Pro Lys Pro Gln Gly
20 25 30
Pro Pro Val Ala Ser Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro Val
35 40 45
Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Leu Leu
50 55 60
Leu Trp Leu Cys Gln Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala
65 70 75 80
Pro Pro Leu Pro Gly His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser
85 90 95
Gly Asp Lys Asp Leu Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly

	100		105		110
Val Gly Leu Cys Glu Glu His Gly Ser Pro Ala Ala Pro Gln His Leu					
	115		120		125
Leu Gly Pro Gly Pro Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr					
	130		135		140
Thr Asp Ile His Thr His Thr His Thr His Ser His Thr His Ser His					
145		150		155	160
Val Glu Gly Lys Val His Gln His Ile His Tyr Gln Cys					
	165		170		

<210> 48
 <211> 1072
 <212> DNA
 <213> Human

<400> 48

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gcccggctgg	gccgcactgt	gcggctgcag	tgcccagtg	agggggaccc	gccgccgctg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggatgacatt	360
agcccaggga	aggagagcct	ggggcccgcg	agctcctctg	ggggtcaaga	ggaccccgcc	420
agccagcagt	gggcacgacc	gcgcttcaca	cagccctcca	agatgaggcg	ccgggtgatc	480
gcacggcccc	tgggtagctc	cgtgcggctc	aagtgcgtgg	ccagcgggca	ccctcggccc	540
gacatcacgt	ggatgaagga	cgaccaggcc	ttgacgcgcc	cagaggccgc	tgagcccagg	600
aagaagaagt	ggacactgag	cctgaagaac	ctgcggccgg	aggacagcgg	caaatacacc	660
tgccgcgtgt	cgaaccgcgc	gggcgccatc	aacgccacct	acaaggtgga	tgtgatccag	720
cggacccggt	ccaagcccgt	gctcacaggc	acgcaccccg	tgaacacgac	ggtggacttc	780
ggggggacca	cgctccttcca	gtgcaaggtg	cgcagcgacg	tgaagccggg	gatccagtgg	840
ctgaagcgcg	tggagtacgg	cgccgagggc	cgccacaact	ccaccatcga	tgtgggcggc	900
cagaagtttg	tggtgctgcc	cacgggtgac	gtgtggtcgc	ggcccgcagg	ctcctacctc	960
aataagctgc	tcatcacccg	tgcccgccag	gacgatgcgg	gcatgtacat	ctgccttggc	1020
gccaacacca	tgggctacag	cttcgcgcag	gccttcctca	ccgtgctgcc	ag	1072

<210> 49
 <211> 357
 <212> PRT
 <213> Human

<400> 49

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu															
1				5					10					15	
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala															
			20					25					30		
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg															
		35					40					45			
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr															
		50				55					60				
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu															
65					70				75						80
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val															
			85					90					95		
Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr															
		100					105					110			
Thr Leu Val Val Leu Asp Asp Ile Ser Pro Gly Lys Glu Ser Leu Gly															
		115				120						125			

Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp
130						135					140				
Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile
145					150					155					160
Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly
				165					170					175	
His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu	Thr
			180					185					190		
Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu
		195					200					205			
Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser
		210				215					220				
Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln
225					230					235					240
Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr
			245						250					255	
Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser
			260					265					270		
Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ala
		275					280					285			
Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val
	290					295				300					
Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu
305					310					315					320
Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr
			325						330					335	
Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe
		340						345					350		
Leu	Thr	Val	Leu	Pro											
		355													

<210> 50
 <211> 718
 <212> DNA
 <213> Human

<400> 50	
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ccggccgccg ccgcccagag ccccccagag atggcggaca aggtgggtccc acggcaggtg	120
gcccggctgg gccgcactgt gcggctgcag tgcccagtgagggggaccc gccgccgctg	180
accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg	240
ccgcaggggc tgaaggatga gcaggtggag cgggaggatg ccggcgtgta cgtgtgcaag	300
gccaccaacg gcttcggcag ccttagcgct aactacaccc tcgtcgtgct ggatgacatt	360
agcccaggga aggagagcct ggggcccagc agctcctctg ggggtcaaga ggaccccgcc	420
agccagcagt gggcacgacc gcgcttcaca cagccctcca agatgaggcg ccgggtgatc	480
gcacggcccc tgggtagctc cgtgcggctc aagtgcgtgg ccagcgggca ccctcggccc	540
gacatcacgt ggatgaagga cgaccaggcc ttgacgcgcc cagaggccgc tgagcccagg	600
aagaagaagt ggacactgag cctgaagaac ctgcggccgg aggacagcgg caaatacacc	660
tgccgcgtgt cgaaccgcgc gggcgccatc aacgccacct acaaggatga tgtgatcc	718

<210> 51
 <211> 239
 <212> PRT
 <213> Human

<400> 51
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu

1	5	10	15
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala			
20	25	30	
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg			
35	40	45	
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr			
50	55	60	
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu			
65	70	75	80
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val			
85	90	95	
Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr			
100	105	110	
Thr Leu Val Val Leu Asp Asp Ile Ser Pro Gly Lys Glu Ser Leu Gly			
115	120	125	
Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp			
130	135	140	
Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val Ile			
145	150	155	160
Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly			
165	170	175	
His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp Asp Gln Ala Leu Thr			
180	185	190	
Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu			
195	200	205	
Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser			
210	215	220	
Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile			
225	230	235	

<210> 52
 <211> 787
 <212> DNA
 <213> Human

<400> 52

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ccggccgccg	ccgcccagag	ccccccaaag	atggcgagaca	aggtgggtccc	acggcagggtg	120
gcccggctgg	gccgcactgt	gcggctgcag	tgcccagtg	agggggaccc	gccgccgctg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggatgacatt	360
agcccaggga	aggagagcct	ggggccccgac	agctcctctg	ggggtcaaga	ggaccccggcc	420
agccagcagt	gggagcggac	ccgttccaag	cccgctgctca	caggcacgca	ccccgtgaac	480
acgacgggtg	acttcggggg	gaccacgtcc	ttccagtgc	aggtgcgcag	cgacgtgaag	540
ccggtgatcc	agtggctgaa	gcgcgtggag	tacggcgccg	agggccgcca	caactccacc	600
atcgatgtgg	gcggccagaa	gtttgtggtg	ctgcccacgg	gtgacgtgtg	gtcgcggccc	660
gacggctcct	acctcaataa	gctgctcatc	acccgtgccc	gccaggacga	tgcgggcatg	720
tacatctgcc	ttggcgccaa	caccatgggc	tacagcttcc	gcagcgcctt	cctcaccgtg	780
ctgccag						787

<210> 53
 <211> 262
 <212> PRT
 <213> Human

<400> 53

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10				15		
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala
			20					25					30		
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
		35					40					45			
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr
	50					55					60				
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
65					70				75						80
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
				85					90					95	
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
			100					105					110		
Thr	Leu	Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly
		115					120					125			
Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp
	130					135					140				
Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn
145					150					155					160
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg
			165						170					175	
Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly
			180					185					190		
Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe
		195					200					205			
Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr
	210					215					220				
Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met
225					230					235					240
Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala
			245						250					255	
Phe	Leu	Thr	Val	Leu	Pro										
			260												

<210> 54
 <211> 991
 <212> DNA
 <213> Human

<400> 54
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 gcccggtgg gccgcactgt gcggctgcag tgcccagtgg agggggaccc gccgccgctg 180
 accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg 240
 ccgcaggggc tgaaggtgaa gcaggtggag cgggaggatg ccggcgtgta cgtgtgcaag 300
 gccaccaacg gcttcggcag ccttagcgtc aactacacc tcgtcgtgct ggcacgaccg 360
 cgcttcacac agccctccaa gatgaggcgc cgggtgatcg cacggcccgt gggtagctcc 420
 gtgcggctca agtgcggtgg cagcgggcac cctcggccc acatcacgtg gatgaaggac 480
 gaccaggcct tgacgcgccc agaggccgct gagcccagga agaagaagtg gacactgagc 540
 ctgaagaacc tgcggccgga ggacagcggc aaatacacct gccgcgtgtc gaaccgcgcg 600
 ggcgccatca acgccaccta caaggtggat gtgateccagc ggacccgttc caagcccgtg 660
 ctcacaggca cgcaccccgt gaacacgacg gtggacttcg gggggaccac gtccttcag 720
 tgcaaggtgc gcagcgacgt gaagccggtg atccagtggc tgaagcgcgt ggagtacggc 780
 gccgagggcc gccacaactc caccatcgat gtgggaggcc agaagtttgt ggtgctgccc 840
 acgggtgacg tgtggtcgcg gcccgacggc tcctacctca ataagctgct catcaccgt 900
 gcccgccagg acgatgcggg catgtacatc tgccttggcg ccaacacat gggctacagc 960

ttccgcagcg ccttcctcac cgtgctgccca g

991

<210> 55
<211> 330
<212> PRT
<213> Human

<400> 55
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
1 5 10 15
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
20 25 30
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
35 40 45
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
50 55 60
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
65 70 75 80
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
85 90 95
Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
100 105 110
Thr Leu Val Val Leu Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met
115 120 125
Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys
130 135 140
Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp
145 150 155 160
Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys
165 170 175
Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr
180 185 190
Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys
195 200 205
Val Asp Val Ile Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr
210 215 220
His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln
225 230 235 240
Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg
245 250 255
Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly
260 265 270
Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro
275 280 285
Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln Asp
290 295 300
Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser
305 310 315 320
Phe Arg Ser Ala Phe Leu Thr Val Leu Pro
325 330

<210> 56
<211> 799
<212> DNA
<213> Human

<400> 56

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tcctctgggg	gtcaagagga	ccccgccagc	cagcagtggg	cacgaccgcg	cttcacacag	180
ccctccaaga	tgaggcgccg	ggtgatcgca	cggcccgtgg	gtagctccgt	gcggctcaag	240
tgcgtaggcca	gcggggcaccc	tcggccccgac	atcacgtgga	tgaaggacga	ccaggccttg	300
acgcgcccag	aggccgctga	gcccaggaag	aagaagtgga	cactgagcct	gaagaacctg	360
cggccggagg	acagcggcaa	atacacctgc	cgcgtgtcga	accgcgcggg	cgccatcaac	420
gccacctaca	aggtggatgt	gatccagcgg	acccgttcca	agcccgtgct	cacaggcacg	480
caccccgtga	acacgacggg	ggacttcggg	gggaccacgt	ccttccagt	caaggtgcgc	540
agcgacgtga	agccggtgat	ccagtggctg	aagcgcgtgg	agtacggcgc	cgagggccgc	600
cacaactcca	ccatcgatgt	gggcggccag	aagtttgtgg	tgctgcccac	gggtgacgtg	660
tggtcgcggc	ccgacggctc	ctacctcaat	aagctgctca	tcacccgtgc	ccgccaggac	720
gatgcgggca	tgtacatctg	ccttggcgcc	aacaccatgg	gctacagctt	ccgcagcgcc	780
ttcctcaccg	tgctgccag					799

<210> 57

<211> 266

<212> PRT

<213> Human

<400> 57

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu	
1				5					10					15		
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	
			20					25					30			
Lys	Glu	Ser	Leu	Gly	Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	
		35					40					45				
Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	
	50					55					60					
Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	
65					70				75						80	
Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp	
			85						90					95		
Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys	
			100					105						110		
Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	
		115					120					125				
Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	
	130					135					140					
Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	
145				150					155						160	
His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	
			165					170						175		
Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	
		180					185						190			
Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	
	195					200						205				
Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	
	210				215						220					
Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp	
225				230					235						240	
Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	
			245				250							255		
Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro							
		260					265									

<210> 58

<211> 433
 <212> DNA
 <213> Human

<400> 58
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 gcccggtctg gccgcactgt gcggctgcag tgcccagtgg aggggggaccc gccgccgctg 180
 accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg 240
 ccgcagggggc tgaagggtgaa gcagggtggag cgggaggatg ccggcgtgta cgtgtgcaag 300
 gccaccaacg gcttcggcag ccttagcgtc aactacaccc tcgtcgtgct ggatgacatt 360
 agcccaggga aggagagcct gggggcccgc agctcctctg ggggtcaaga ggaccccgcc 420
 agccagcagt ggg 433

<210> 59
 <211> 144
 <212> PRT
 <213> Human

<400> 59
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
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 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
 20 25 30
 Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
 35 40 45
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
 50 55 60
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
 65 70 75 80
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
 85 90 95
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100 105 110
 Thr Leu Val Val Leu Asp Asp Ile Ser Pro Gly Lys Glu Ser Leu Gly
 115 120 125
 Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp
 130 135 140

<210> 60
 <211> 637
 <212> DNA
 <213> Human

<400> 60
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 ccggccgccg ccgcccagg ccccccaaag atggcggaca aggtgggtccc acggcagggtg 120
 gcccggtctg gccgcactgt gcggctgcag tgcccagtgg aggggggaccc gccgccgctg 180
 accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg 240
 ccgcagggggc tgaagggtgaa gcagggtggag cgggaggatg ccggcgtgta cgtgtgcaag 300
 gccaccaacg gcttcggcag ccttagcgtc aactacaccc tcgtcgtgct ggcacgaccg 360
 cgcttcacac agccctccaa gatgaggcgc cgggtgatcg cacggcccgt gggtagctcc 420
 gtgcggctca agtgcgtggc cagcgggcac cctcggccc acatcacgtg gatgaaggac 480
 gaccaggcct tgacgcgccc agaggccgct gagcccagga agaagaagtg gacactgagc 540
 ctgaagaacc tgcggccgga ggacagcggc aaatacacct gccgcgtgtc gaaccgcgcg 600
 ggcgccatca acgccaccta caagggtgat gtgatcc 637

<210> 61
 <211> 212
 <212> PRT
 <213> Human

<400> 61

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10				15		
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala
			20					25					30		
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
		35					40					45			
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr
	50					55					60				
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
65					70				75					80	
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
				85					90					95	
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
			100					105					110		
Thr	Leu	Val	Val	Leu	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met
		115					120					125			
Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys
	130					135						140			
Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp
145					150					155				160	
Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys
				165					170					175	
Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr
			180					185					190		
Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys
		195					200					205			
Val	Asp	Val	Ile												
			210												

<210> 62
 <211> 706
 <212> DNA
 <213> Human

<400> 62

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gcccggctgg	gccgcactgt	gcggctgcag	tgcccagtg	agggggaccc	gccgccgctg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaagggtgaa	gcaggtggag	cgaggagatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggagcggacc	360
cgttccaagc	ccgtgctcac	aggcacgcac	cccgtgaaca	cgacgggtgga	cttcgggggg	420
accacgtcct	tccagtgcaa	ggtgcgcagc	gacgtgaagc	cggatgatcca	gtggctgaag	480
cgcgtggagt	acggcgccga	gggccgccac	aactccacca	tcgatgtggg	cggccagaag	540
tttgtggtgc	tgcccacggg	tgacgtgtgg	tcgcggcccc	acggctccta	cctcaataag	600
ctgctcatca	cccgtgcccc	ccaggacgat	gcgggcatgt	acatctgcct	tggcgccaac	660
accatgggct	acagcttccg	cagcgccttc	ctcaccgtgc	tgccag		706

<210> 63
 <211> 235
 <212> PRT

<213> Human

<400> 63

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Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1          5          10          15
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
          20          25          30
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
          35          40          45
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
          50          55          60
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
65          70          75          80
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
          85          90          95
Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
          100          105          110
Thr Leu Val Val Leu Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly
          115          120          125
Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe
          130          135          140
Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys
145          150          155          160
Arg Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val
          165          170          175
Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg
          180          185          190
Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln
          195          200          205
Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr
          210          215          220
Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro
225          230          235
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<210> 64

<211> 445

<212> DNA

<213> Human

<400> 64

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ccggccgccg ccgcccgaga tgacattagc ccagggaagg agagcctggg gcccgacagc      120
tcctctgggg gtcaagagga ccccgccagc cagcagtggg cacgaccgcg cttcacacag      180
ccctccaaga tgaggcgccg ggtgatcgca cggcccgtgg gtagctccgt gcggctcaag      240
tgcgtaggcca gcgggcaccc tcggcccagc atcacgtgga tgaaggacga ccaggccttg      300
acgcgcccag aggccgctga gcccgaggaag aagaagtgga cactgagcct gaagaacctg      360
cggccggagg acagcggcaa atacacctgc cgcgtgtcga accgcgcggg cgccatcaac      420
gccacctaca aggtggatgt gatcc                                     445
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<210> 65

<211> 148

<212> PRT

<213> Human

<400> 65

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Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1          5          10          15
```

Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly
			20					25					30		
Lys	Glu	Ser	Leu	Gly	Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro
		35					40					45			
Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met
	50					55					60				
Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys
65					70					75					80
Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp
				85					90					95	
Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys
			100					105					110		
Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr
		115					120					125			
Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys
	130					135					140				
Val	Asp	Val	Ile												
145															

<210> 66

<211> 514

<212> DNA

<213> Human

<400> 66

atgacgccga	gccccctggt	gctgctcctg	ctgccgccgc	tgctgctggg	ggccttccca	60
ccggccgccg	ccgcccagaga	tgacattagc	ccagggaagg	agagcctggg	gcccagacagc	120
tcctctgggg	gtcaagagga	ccccgccagc	cagcagtggg	agcggacccg	ttccaagccc	180
gtgctcacag	gcacgcaccc	cgtgaacacg	acggtggact	tcggggggac	cacgtccttc	240
cagtgcgaagg	tgcgacagca	cgtgaagccg	gtgatccagt	ggctgaagcg	cgtggagtac	300
ggcgccgagg	gccgccacaa	ctccaccatc	gatgtgggcg	gccagaagtt	tgtggtgctg	360
cccacgggtg	acgtgtggtc	gcggccccgac	ggctcctacc	tcaataagct	gctcatcacc	420
cgtgcccgcc	aggacgatgc	gggcatgtac	atctgccttg	gcgccaacac	catgggctac	480
agcttccgca	gcgccttcct	caccgtgctg	ccag			514

<210> 67

<211> 171

<212> PRT

<213> Human

<400> 67

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10					15	
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly
			20					25					30		
Lys	Glu	Ser	Leu	Gly	Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro
		35					40					45			
Ala	Ser	Gln	Gln	Trp	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly
	50					55					60				
Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe
65					70					75					80
Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys
				85					90					95	
Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val
			100					105					110		
Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg
		115					120					125			

Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln
130						135					140				
Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr
145				150					155						160
Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro					
			165						170						

<210> 68
 <211> 718
 <212> DNA
 <213> Human

<400> 68

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ccggccgccg	ccgcccgagc	acgaccgcgc	ttcacacagc	cctccaagat	gaggcgccgg	120
gtgatcgcac	ggcccgtggg	tagctccgtg	cggctcaagt	gcgtggccag	cgggcaccct	180
cggcccgcaca	tcacgtggat	gaaggacgac	caggccttga	cgcgcccaga	ggccgctgag	240
cccaggaaga	agaagtggac	actgagcctg	aagaacctgc	ggccggagga	cagcggcaaa	300
tacacctgcc	gcgtgtcgaa	ccgcgcgggc	gccatcaacg	ccacctacaa	ggtggatgtg	360
atccagcgga	cccgttccaa	gcccggtgctc	acaggcacgc	accccgtgaa	cacgacgggtg	420
gacttcgggg	ggaccacgtc	cttccagtgc	aagggtgcga	gcgacgtgaa	gccgggtgatc	480
cagtggctga	agcgcgtgga	gtacggcgcc	gagggccgcc	acaactccac	catcgatgtg	540
ggcggccaga	agtttgtggt	gctgcccacg	ggtgacgtgt	ggtcgcggcc	cgacggctcc	600
tacctcaata	agctgctcat	cacccggtgcc	cgccaggacg	atgcgggcat	gtacatctgc	660
cttggcgcca	acaccatggg	ctacagcttc	cgcagcgcct	tcctcaccgt	gctgccag	718

<210> 69
 <211> 239
 <212> PRT
 <213> Human

<400> 69

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10					15	
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Ala	Arg	Pro	Arg	Phe	Thr
			20					25					30		
Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser
		35					40					45			
Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile
	50					55					60				
Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu
65					70					75					80
Pro	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu
			85						90					95	
Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile
			100					105					110		
Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro
			115				120					125			
Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly
	130					135					140				
Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile
145					150					155					160
Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser
			165					170						175	
Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp
			180					185					190		
Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr

	195		200		205
Arg	Ala Arg Gln Asp Asp	Ala Gly Met Tyr Ile	Cys Leu Gly Ala Asn		
210		215	220		
Thr Met Gly Tyr Ser Phe	Arg Ser Ala Phe Leu	Thr Val Leu Pro			
225	230	235			

<210> 70
 <211> 352
 <212> DNA
 <213> Human

<400> 70
 atgacgccga gccccctggt gctgctcctg ctgccgccgc tgctgctggg ggccttccca 60
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 gcccggtctg gccgcactgt gcggctgcag tgcccagtgg agggggaccc gccgccgctg 180
 accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg 240
 ccgcagggggc tgaaggatgaa gcagggtggag cgggaggatg ccggcgtgta cgtgtgcaag 300
 gccaccaacg gcttcggcag ccttagcgtc aactacaccc tcgtcgtgct gg 352

<210> 71
 <211> 117
 <212> PRT
 <213> Human

<400> 71
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1 5 10 15
 Gly Ala Phe Pro Pro Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
 20 25 30
 Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
 35 40 45
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
 50 55 60
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
 65 70 75 80
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
 85 90 95
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100 105 110
 Thr Leu Val Val Leu
 115

<210> 72
 <211> 160
 <212> DNA
 <213> Human

<400> 72
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 ccggccgccg ccgcccagaga tgacattagc ccagggaagg agagcctggg gcccgacagc 120
 tcctctgggg gtcaagagga ccccgccagc cagcagtggg 160

<210> 73
 <211> 53
 <212> PRT
 <213> Human

<400> 73

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
1 5 10 15
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly
20 25 30
Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro
35 40 45
Ala Ser Gln Gln Trp
50

<210> 74

<211> 364

<212> DNA

<213> Human

<400> 74

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gtgatcgcac ggcccgtggg tagctccgtg cggctcaagt gcgtggccag cgggcaccct 180
cggcccgcaca tcacgtggat gaaggacgac caggccttga cgcgcccaga ggccgctgag 240
cccaggaaga agaagtggac actgagcctg aagaacctgc ggccggagga cagcggcaaa 300
tacacctgcc gcgtgtcgaa ccgcgcgggc gccatcaacg ccacctacaa ggtggatgtg 360
atcc 364

<210> 75

<211> 121

<212> PRT

<213> Human

<400> 75

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
1 5 10 15
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Ala Arg Pro Arg Phe Thr
20 25 30
Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser
35 40 45
Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile
50 55 60
Thr Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu
65 70 75 80
Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu
85 90 95
Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile
100 105 110
Asn Ala Thr Tyr Lys Val Asp Val Ile
115 120

<210> 76

<211> 433

<212> DNA

<213> Human

<400> 76

atgacgccga gccccctggt gctgctcctg ctgccgccgc tgctgctggg ggccttccca 60
ccggccgccg ccgcccgcgc gcggaccggt tccaagcccg tgctcacagg cagcaccgcc 120
gtgaacacga cgggtggactt cgggggggacc acgtccttcc agtgcaagggt gcgcagcgac 180
gtgaagccgg tgatccagtg gctgaagcgc gtggagtacg gcgccgaggg ccgccacaac 240

tccaccatcg atgtgggagg ccagaagttt gtgggtgctgc ccacgggtga cgtgtgggtcg	300
cggcccgacg gctcctacct caataagctg ctcacacccc gtgcccggca ggacgatgag	360
ggcatgtaca tctgccttgg cgccaacacc atggggtaca gcttccgcag cgccttcctc	420
accgtgctgc cag	433

<210> 77
 <211> 144
 <212> PRT
 <213> Human

<400> 77

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10					15	
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Glu	Arg	Thr	Arg	Ser	Lys
			20				25						30		
Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly
		35					40					45			
Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val
	50					55					60				
Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn
65					70					75					80
Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly
			85						90					95	
Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile
			100					105					110		
Thr	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala
		115					120					125			
Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro
	130					135					140				

<210> 78
 <211> 79
 <212> DNA
 <213> Human

<400> 78	
atgacgccga gccccctgtt gctgctcctg ctgccggcgc tgctgctggg ggccttccca	60
ccggccggcg ccgcccag	79

<210> 79
 <211> 26
 <212> PRT
 <213> Human

<400> 79

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10					15	
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg						
			20					25							

<210> 80
 <211> 1590
 <212> DNA
 <213> Mouse

<400> 80	
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gcgcgaggac	ccccagaat	ggcagacaaa	gtggtccac	ggcaggtggc	ccgcctgggc	120
cgcactgtgc	ggctacagtg	cccagtgag	ggggaccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccaggggtctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccaggggaag	360
gagagccctg	ggccaggtgg	ttcttcgggg	ggccaggagg	accagccag	ccagcagtg	420
gcacggcctc	gcttcacaca	gccctccaag	atgaggcgcc	gagtgattgc	acggcctgtg	480
ggtagctctg	tgcggctcaa	gtgtgtggcc	agtgggcacc	cacggccaga	catcatgtgg	540
atgaaggatg	accagacctt	gacgcatcta	gaggctagt	aacacagaaa	gaagaagtgg	600
acactgagct	tgaagaacct	gaagcctgaa	gacagtggca	agtacacgtg	ccgtgtatct	660
aacaaggccg	gtgccatcaa	cgccacctac	aaagtggatg	taatccagcg	gactcgttcc	720
aagcctgtgc	tcacagggac	acaccctgtg	aacacaacgg	tggacttcgg	tgggacaacg	780
tccttccagt	gcaaggtg	cagtgtgac	aagcctgtga	tccagtggct	gaagcgggtg	840
gagtacggct	ccgagggacg	ccacaactcc	accattgatg	tgggtggcca	gaagtttgtg	900
gtgttgccca	cgggtgatgt	gtggtcacgg	cctgatggct	cctacctcaa	caagctgctc	960
atctctcggg	cccgccagga	tgatgctggc	atgtacatct	gcctaggtgc	aaataccatg	1020
ggctacagtt	tccgtagcgc	cttcctcact	gtattaccag	accccaaacc	tccagggcct	1080
cctatggctt	cttcacgtc	atccacaagc	ctgccatggc	ctgtggtgat	cggcatccca	1140
gctggtgctg	tcttcacct	aggcactgtg	ctgctctggc	tttgccagac	caagaagaag	1200
ccatgtgccc	cagcatctac	acttcctgtg	cctgggcac	gtcccccagg	gacatcccga	1260
gaacgcagtg	gtgacaagga	cctgccctca	ttggctgtgg	gcatatgtga	ggagcatgga	1320
tccgccatgg	ccccccagca	catcctggcc	tctggctcaa	ctgctggccc	caagctgtac	1380
cccaagctat	acacagatgt	gcacacacac	acacatacac	acacctgcac	tcacacgctc	1440
tcatgtggag	ggcaagggttc	atcaacacca	gcatgtccac	tatcagtgtc	aaatacagcg	1500
aatctccaag	cactgtgtcc	tgaggtaggc	atttgggggc	caaggcaaca	ggttgggaga	1560
attgagaaca	atggaggaag	agtatcttag				1590

<210> 81

<211> 529

<212> PRT

<213> Mouse

<400> 81

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1				5				10					15	
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val
			20				25					30		Val
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys
		35				40					45			Pro
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly
	50					55				60				Arg
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly
65					70				75					80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys
			85					90				95		Lys
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile
		100						105				110		Ile
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly
	115						120					125		Ser
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro
	130					135					140			Arg
Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro
145					150					155				160
Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg
			165					170				175		Pro
Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu
		180						185					190	Ala

Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys	
		195					200					205				
Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly	
	210					215					220					
Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	
225					230					235					240	
Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	
			245						250					255		
Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	
			260					265					270			
Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg	His	
		275					280					285				
Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	
	290					295					300					
Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	
305					310					315					320	
Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	
			325						330					335		
Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	
			340					345					350			
Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser	
	355					360						365				
Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	
	370					375					380					
Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	
385					390					395					400	
Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro	
			405						410					415		
Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	
			420					425					430			
Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile	
	435						440					445				
Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	
	450					455					460					
Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu	
465					470					475					480	
Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val	
			485					490					495			
Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp	
		500						505					510			
Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val	
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Ser																

<210> 82
 <211> 1236
 <212> DNA
 <213> Mouse

<400> 82	
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cgcactgtgc ggctacagtg cccagtggag ggggaccac caccgttgac catgtggacc	180
aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggtctg	240
aaggtgaagg aggtggaggc cgaggatgcc ggtgtttatg tgtgcaaggc caccaatggc	300
tttggcagcc tcagcgtcaa ctacactctc atcatcatgg atgatattag tccagggaag	360

gagagccctg	ggccaggtgg	ttcttcgggg	ggccaggagg	acccagccag	ccagcagtgg	420
gcacggcctc	gcttcacaca	gccctccaag	atgaggcgcc	gagtgattgc	acggcctgtg	480
ggtagctctg	tgcggctcaa	gtgtgtggcc	agtgggcacc	cacggccaga	catcatgtgg	540
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acgctctcat	gtggagggca	aggttcatca	acaccagcat	gtccactatc	agtgtctaat	1140
acagcgaatc	tccaagcact	gtgtcctgag	gtaggcattt	gggggccaag	gcaacagggt	1200
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<210> 83

<211> 411

<212> PRT

<213> Mouse

<400> 83

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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			20				25					30		Val
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys
		35					40					45		Pro
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly
	50					55					60			Arg
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly
65					70				75					80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys
			85					90				95		Lys
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile
		100					105					110		Ile
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly
	115					120					125			Ser
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro
	130					135					140			Arg
Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro
145					150					155				160
Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg
			165						170				175	Pro
Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu
	180							185					190	Ala
Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu
	195						200					205		Lys
Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala
	210					215						220		Gly
Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	His	Pro	Lys	Pro
225					230					235				240
Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp
			245						250				255	Pro
Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr
		260					265					270		Val
Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala
														Ser

275	280	285
Thr Leu Pro Val Pro Gly His Arg Pro Pro Gly Thr Ser Arg Glu Arg		
290	295	300
Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Val Gly Ile Cys Glu Glu		
305	310	315
His Gly Ser Ala Met Ala Pro Gln His Ile Leu Ala Ser Gly Ser Thr		
	325	330
Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Val His Thr His		
	340	345
Thr His Thr His Thr Cys Thr His Thr Leu Ser Cys Gly Gly Gln Gly		
	355	360
Ser Ser Thr Pro Ala Cys Pro Leu Ser Val Leu Asn Thr Ala Asn Leu		
370	375	380
Gln Ala Leu Cys Pro Glu Val Gly Ile Trp Gly Pro Arg Gln Gln Val		
385	390	395
Gly Arg Ile Glu Asn Asn Gly Gly Arg Val Ser		
	405	410

<210> 84
 <211> 1305
 <212> DNA
 <213> Mouse

<400> 84

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cgcactgtgc	ggctacagt	cccagtgag	ggggaccac	caccgttgac	catgtggacc	180
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gagagccctg	ggccaggtgg	ttcttcgggg	ggccaggagg	accagccag	ccagcagtgg	420
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ttcgggtggga	caacgtcctt	ccagtgcgaag	gtgcgcagtg	acgtgaagcc	tgtgatccag	540
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ggccagaagt	ttgtggtgtt	gcccacgggt	gatgtgtggt	cacggcctga	tggctcctac	660
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aaacctccag	ggcctcctat	ggcttcttca	tcgtcatcca	caagcctgcc	atggcctgtg	840
gtgatcggca	tcccagctgg	tgctgtcttc	atcctaggca	ctgtgctgct	ctggccttgc	900
cagaccaaga	agaagccatg	tgccccagca	tctacacttc	ctgtgcctgg	gcatcgtccc	960
ccagggacat	cccgagaacg	cagtgggtgac	aaggacctgc	cctcattggc	tgtgggcata	1020
tgtgaggagc	atggatccgc	catggccccc	cagcacatcc	tggcctctgg	ctcaactgct	1080
ggccccaagc	tgtaccccaa	gctatacaca	gatgtgcaca	cacacacaca	tacacacacc	1140
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gtgctaaata	cagcgaatct	ccaagcactg	tgtcctgagg	taggcatttg	ggggccaagg	1260
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<210> 85
 <211> 434
 <212> PRT
 <213> Mouse

<400> 85

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro
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Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
20 25 30

<213> Mouse

<400> 86

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cgcactgtgc	ggctacagtg	cccagtggag	ggggacccac	caccgttgac	catgtggacc	180
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cacacacaca	cacatacaca	cacctgcact	cacacgctct	catgtggagg	gcaaggttca	1380
tcaacaccag	catgtccact	atcagtgcta	aatacagcga	atctccaagc	actgtgtcct	1440
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gtatcttag						1509

<210> 87

<211> 502

<212> PRT

<213> Mouse

<400> 87

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
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Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
			20					25					30		
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
			35				40					45			
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
	50					55				60					
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
65					70				75						80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
			85					90						95	
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
			100					105					110		
Met	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val
		115					120					125			
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser
	130					135						140			
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu
145					150					155					160
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser

				165					170					175			
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val		
			180					185					190				
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile		
		195					200					205					
Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn		
	210					215					220						
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg		
225					230				235						240		
Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly		
			245					250					255				
Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe		
		260					265						270				
Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr		
	275					280					285						
Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met		
	290					295					300						
Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala		
305				310					315						320		
Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala		
			325					330						335			
Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile		
		340					345						350				
Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys		
	355					360					365						
Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro		
	370				375						380						
Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp		
385				390					395						400		
Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met		
			405					410						415			
Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu		
		420					425						430				
Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr		
	435					440					445						
Cys	Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala		
	450				455						460						
Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro		
465					470					475					480		
Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn		
			485					490						495			
Asn	Gly	Gly	Arg	Val	Ser												
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<210> 88
 <211> 1317
 <212> DNA
 <213> Mouse

<400> 88

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gctagtgaac	acagaaagaa	gaagtggaca	ctgagcttga	agaacctgaa	gcctgaagac	360
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<210> 89

<211> 438

<212> PRT

<213> Mouse

<400> 89

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			20					25					30		
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln
			35				40					45			
Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val
	50					55					60				
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser
65					70					75					80
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu
				85					90					95	
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser
			100					105					110		
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val
		115					120					125			
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile
	130					135					140				
Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn
145					150					155					160
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg
			165					170						175	
Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly
			180					185					190		
Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe
	195						200					205			
Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr
	210					215					220				
Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met
225					230					235					240
Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala
			245					250						255	
Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala
			260					265					270		
Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile

	275		280		285										
Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys
	290					295					300				
Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro
305					310					315					320
Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp
			325						330					335	
Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met
		340						345					350		
Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu
	355						360					365			
Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr
370						375					380				
Cys	Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala
385					390					395					400
Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro
			405						410					415	
Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn
		420					425					430			
Asn	Gly	Gly	Arg	Val	Ser										
	435														

<210> 90

<211> 951

<212> DNA

<213> Mouse

<400> 90

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cgcactgtgc	ggctacagt	cccagtggag	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccaggggtctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccagggaag	360
gagagccctg	ggccagggtg	ttcttcgggg	ggccaggagg	acccagccag	ccagcagtgg	420
gaccccaaac	ctccagggcc	tcctatggct	tcttcatcgt	catccacaag	cctgccatgg	480
cctgtggtga	tcggcatccc	agctgggtgct	gtcttcatcc	taggcactgt	gctgctctgg	540
ctttgccaga	ccaagaagaa	gcatgtgcc	ccagcatcta	cacttcctgt	gcctgggcat	600
cgtccccccag	ggacatccc	agaacgcagt	ggtgacaagg	acctgccctc	attggctgtg	660
ggcatatgtg	aggagcatgg	atccgccatg	gccccccagc	acatcctggc	ctctgggtca	720
actgctggcc	ccaagctgta	ccccaaagcta	tacacagatg	tgcacacaca	cacacataca	780
cacacctgca	ctcacacgct	ctcatgtgga	gggcaagggt	catcaacacc	agcatgtcca	840
ctatcagtgc	taaatacagc	gaatctccaa	gcactgtgtc	ctgaggtagg	catttggggg	900
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<210> 91

<211> 316

<212> PRT

<213> Mouse

<400> 91

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
			20				25					30			
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro

	35		40		45
Val	Glu Gly Asp Pro Pro Pro	Leu Thr Met Trp	Thr Lys Asp Gly Arg		
50		55	60		
Thr	Ile His Ser Gly Trp	Ser Arg Phe Arg	Val Leu Pro Gln Gly Leu		
65		70	75		80
Lys	Val Lys Glu Val Glu Ala Glu Asp	Ala Gly Val Tyr Val Cys Lys			
	85	90	95		
Ala	Thr Asn Gly Phe Gly Ser Leu Ser	Val Asn Tyr Thr Leu Ile Ile			
	100	105	110		
Met	Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly	Pro Gly Gly Ser			
	115	120	125		
Ser	Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln	Trp Asp Pro Lys Pro			
	130	135	140		
Pro	Gly Pro Pro Met Ala Ser Ser Ser Ser	Thr Ser Leu Pro Trp			
145		150	155		160
Pro	Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr				
	165	170	175		
Val	Leu Leu Trp Leu Cys Gln Thr Lys Lys Lys	Pro Cys Ala Pro Ala			
	180	185	190		
Ser	Thr Leu Pro Val Pro Gly His Arg Pro Pro Gly	Thr Ser Arg Glu			
	195	200	205		
Arg	Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Val Gly Ile Cys Glu				
	210	215	220		
Glu	His Gly Ser Ala Met Ala Pro Gln His Ile Leu Ala Ser Gly Ser				
225		230	235		240
Thr	Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Val His Thr				
	245	250	255		
His	Thr His Thr His Thr Cys Thr His Thr Leu Ser Cys Gly Gly Gln				
	260	265	270		
Gly	Ser Ser Thr Pro Ala Cys Pro Leu Ser Val Leu Asn Thr Ala Asn				
	275	280	285		
Leu	Gln Ala Leu Cys Pro Glu Val Gly Ile Trp Gly Pro Arg Gln Gln				
	290	295	300		
Val	Gly Arg Ile Glu Asn Asn Gly Gly Arg Val Ser				
305		310	315		

<210> 92
 <211> 1155
 <212> DNA
 <213> Mouse

<400> 92

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cgcactgtgc	ggctacagt	cccagtgag	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggtctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	cacggcctcg	cttcacacag	360
ccctccaaga	tgaggcgccg	agtgattgca	cggcctgtgg	gtagctctgt	gcggctcaag	420
tgtgtggcca	gtgggcaccc	acggccagac	atcatgtgga	tgaaggatga	ccagaccttg	480
acgcacttag	aggctagtga	acacagaaag	aagaagtgga	cactgagctt	gaagaacctg	540
aagcctgaag	acagtggcaa	gtacacgtgc	cgtgtatcta	acaaggccgg	tgccatcaac	600
gccacctaca	aagtggatgt	aatccacccc	aaacctccag	ggcctcctat	ggcttcttca	660
tcgtcatcca	caagcctgcc	atggcctgtg	gtgatcggca	tcccagctgg	tgctgtcttc	720
atcctaggca	ctgtgctgct	ctggctttgc	cagaccaaga	agaagccatg	tgccccagca	780
tctacacttc	ctgtgcctgg	gcatcgtccc	ccagggacat	cccgagaacg	cagtggtgac	840
aaggacctgc	cctcattggc	tgtgggcata	tgtgaggagc	atggatccgc	catggccccc	900

cagcacatcc	tggcctctgg	ctcaactgct	ggccccaagc	tgtaccccaa	gctatacaca	960
gatgtgcaca	cacacacaca	tacacacacc	tgcactcaca	cgctctcatg	tggagggcaa	1020
ggttcatcaa	caccagcatg	tccactatca	gtgctaaata	cagcgaatct	ccaagcactg	1080
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ggaagagtat	cttag					1155

<210> 93
 <211> 384
 <212> PRT
 <213> Mouse

<400> 93

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
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Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val	
			20				25						30			
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro	
		35					40					45				
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg	
	50					55					60					
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu	
65				70					75						80	
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys	
			85					90						95		
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile	
		100					105						110			
Met	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	
		115					120					125				
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	
	130				135						140					
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	
145					150					155					160	
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	
			165					170						175		
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	
		180					185						190			
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	
	195					200						205				
His	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser	Thr	
	210				215						220					
Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	
225				230						235					240	
Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	Pro	
			245						250					255		
Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro	Gly	
		260					265						270			
Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Val	
		275					280					285				
Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile	Leu	
	290					295					300					
Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	
305					310					315					320	
Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu	Ser	
			325						330					335		
Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val	Leu	
		340					345					350				
Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp	Gly	

	355		360		365										
Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val	Ser
	370					375					380				

<210> 94
 <211> 1224
 <212> DNA
 <213> Mouse

<400> 94

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cgcactgtgc	ggctacagt	cccagtgagg	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggtctg	240
aagggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	agcggactcg	ttccaagcct	360
gtgctcacag	ggacacaccc	tgtgaacaca	acggtggact	tcggtgggac	aacgtccttc	420
cagtgaagg	tgcgcagtga	cgtgaagcct	gtgatccagt	ggctgaagcg	ggtggagtac	480
ggctccgagg	gacgccacaa	ctccaccatt	gatgtgggtg	gccagaagtt	tgtgggtgtg	540
cccacgggtg	atgtgtggtc	acggcctgat	ggctcctacc	tcaacaagct	gctcatctct	600
cgggcccggc	aggatgatgc	tggcatgtac	atctgcctag	gtgcaaatac	catgggctac	660
agtttccgta	gcgccttcct	cactgtatta	ccagacccca	aacctccagg	gcctcctatg	720
gcttcttcat	cgtcatccac	aagcctgcca	tggcctgtgg	tgatcggcat	cccagctggt	780
gctgtcttca	tcctaggcac	tgtgctgctc	tggctttgcc	agaccaagaa	gaagccatgt	840
gccccagcat	ctacacttcc	tgtgcctggg	catcgtcccc	cagggacatc	ccgagaacgc	900
agtggtgaca	aggacctgcc	ctcattggct	gtgggcatat	gtgaggagca	tggatccgcc	960
atggccccc	agcacatcct	ggcctctggc	tcaactgctg	gccccaaagt	gtaccccaag	1020
ctatacacag	atgtgcacac	acacacacat	acacacacct	gcactcacac	gctctcatgt	1080
ggagggcaag	gttcatcaac	accagcatgt	ccactatcag	tgctaaatac	agcgaatctc	1140
caagcactgt	gtcctgaggt	aggcatttgg	gggccaaggc	aacaggttgg	gagaattgag	1200
aacaatggag	gaagagtatc	ttag				1224

<210> 95
 <211> 407
 <212> PRT
 <213> Mouse

<400> 95

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val
			20				25					30		
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys
		35				40					45			
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly
	50					55					60			
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly
65				70				75					80	
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys
			85					90					95	
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile
		100					105					110		
Met	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro
		115					120					125		
Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys
	130					135					140			
Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu
														Tyr

145					150					155				160	
Gly	Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys
				165					170					175	
Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser
			180					185					190		
Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly
		195					200					205			
Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser
	210					215					220				
Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met
225				230						235					240
Ala	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly
				245				250						255	
Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu
			260				265						270		
Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val
		275					280					285			
Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys
	290					295					300				
Asp	Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala
305					310					315					320
Met	Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys
			325					330						335	
Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His
			340					345					350		
Thr	Cys	Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro
		355					360					365			
Ala	Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys
	370					375					380				
Pro	Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu
385					390				395						400
Asn	Asn	Gly	Gly	Arg	Val	Ser									
				405											

<210> 96
 <211> 963
 <212> DNA
 <213> Mouse

<400> 96

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caggaggacc	cagccagcca	gcagtgggca	cggcctcgct	tcacacagcc	ctccaagatg	180
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gggcacccac	ggccagacat	catgtggatg	aaggatgacc	agaccttgac	gcatctagag	300
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agtggcaagt	acacgtgccg	tgtatctaac	aaggccggtg	ccatcaacgc	cacctacaaa	420
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ggcatttggg	ggccaaggca	acaggttggg	agaattgaga	acaatggagg	aagagtatct	960
tag						963

acacaccctg	tgaacacaac	ggtggacttc	ggtgggacaa	cgtccttcca	gtgcaaggtg	240
cgcagtgcg	tgaagcctgt	gatccagtgg	ctgaagcggg	tggagtacgg	ctccgagggg	300
cgccacaact	ccaccattga	tgtgggtggc	cagaagtttg	tgggtgttgcc	cacgggtgat	360
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gccttcctca	ctgtattacc	agaccccaaa	cctccagggc	ctcctatggc	ttcttcatcg	540
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acacttcctg	tgctggggca	tcgtcccca	gggacatccc	gagaacgcag	tggtgacaag	720
gacctgccct	cattggctgt	gggcatatgt	gaggagcatg	gatccgccat	ggccccccag	780
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gtgcacacac	acacacatac	acacacctgc	actcacacgc	tctcatgtgg	agggcaaggt	900
tcatcaacac	cagcatgtcc	actatcagtg	ctaaatacag	cgaatctcca	agcactgtgt	960
cctgaggtag	gcatttgggg	gccaaggcaa	caggttggga	gaattgagaa	caatggagga	1020
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<210> 99
 <211> 343
 <212> PRT
 <213> Mouse

<400> 99

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
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Ser	Ala	Glu	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
			20					25					30		
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln
			35				40						45		
Trp	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val
	50					55					60				
Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val
65					70					75					80
Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr
				85				90						95	
Gly	Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys
			100					105						110	
Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser
			115				120					125			
Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly
	130					135					140				
Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser
145				150						155					160
Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met
				165					170					175	
Ala	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly
			180					185						190	
Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu
		195					200					205			
Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val
	210					215					220				
Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys
225					230					235					240
Asp	Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala
				245					250					255	
Met	Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys
			260					265					270		
Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His

			100					105					110				
Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly		
		115						120					125				
Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe		
		130						135					140				
Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys		
145					150					155					160		
Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val		
				165					170					175			
Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg		
			180					185					190				
Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln		
		195					200					205					
Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr		
		210				215					220						
Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro		
225					230					235					240		
Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro		
				245				250						255			
Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val		
			260					265					270				
Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser		
		275				280					285						
Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg		
		290				295					300						
Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu		
305					310					315					320		
His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr		
				325				330						335			
Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His		
			340					345					350				
Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln	Gly		
		355					360					365					
Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu		
		370				375					380						
Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val		
385					390					395					400		
Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val	Ser							
				405				410									

<210> 102
 <211> 870
 <212> DNA
 <213> Mouse

<400> 102

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cgcactgtgc	ggctacagt	cccagtgag	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggtctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	accccaaacc	tccagggcct	360
cctatggctt	cttcacgtc	atccacaagc	ctgccatggc	ctgtgggtgat	cggcatccca	420
gctggtgctg	tcttcacct	aggcactgtg	ctgctctggc	tttgccagac	caagaagaag	480
ccatgtgccc	cagcatctac	acttcctgtg	cctgggcatc	gtcccccagg	gacatcccga	540
gaacgcagt	gtgacaagga	cctgccctca	ttggctgtgg	gcatatgtga	ggagcatgga	600
tccgccatgg	ccccccagca	catcctggcc	tctggctcaa	ctgctggccc	caagctgtac	660

cccaagctat acacagatgt gcacacacac acacatacac acacctgcac tcacacgctc	720
tcatgtggag ggcaagggtc atcaacacca gcatgtccac tatcagtgtt aaatacagcg	780
aatctccaag cactgtgtcc tgaggtaggc atttgggggc caaggcaaca ggttgggaga	840
attgagaaca atggaggaag agtatcttag	870

<210> 103
 <211> 289
 <212> PRT
 <213> Mouse

<400> 103

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro	
1 5 10 15	
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val	
20 25 30	
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro	
35 40 45	
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg	
50 55 60	
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu	
65 70 75 80	
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys	
85 90 95	
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile	
100 105 110	
Met Asp Pro Lys Pro Pro Gly Pro Pro Met Ala Ser Ser Ser Ser Ser	
115 120 125	
Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val	
130 135 140	
Phe Ile Leu Gly Thr Val Leu Leu Trp Leu Cys Gln Thr Lys Lys Lys	
145 150 155 160	
Pro Cys Ala Pro Ala Ser Thr Leu Pro Val Pro Gly His Arg Pro Pro	
165 170 175	
Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala	
180 185 190	
Val Gly Ile Cys Glu Glu His Gly Ser Ala Met Ala Pro Gln His Ile	
195 200 205	
Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr	
210 215 220	
Thr Asp Val His Thr His Thr His Thr His Thr Cys Thr His Thr Leu	
225 230 235 240	
Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro Ala Cys Pro Leu Ser Val	
245 250 255	
Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys Pro Glu Val Gly Ile Trp	
260 265 270	
Gly Pro Arg Gln Gln Val Gly Arg Ile Glu Asn Asn Gly Gly Arg Val	
275 280 285	

Ser

<210> 104
 <211> 678
 <212> DNA
 <213> Mouse

<400> 104

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caggaggacc	cagccagcca	gcagtgggac	cccaaacctc	cagggcctcc	tatggcttct	180
tcatcgtcat	ccacaagcct	gccatggcct	gtggtgatcg	gcatcccagc	tggtgctgtc	240
ttcatcctag	gcactgtgct	gctctggcct	tgccagacca	agaagaagcc	atgtgcccga	300
gcatctacac	ttcctgtgcc	tgggcatcgt	ccccagggga	catcccagaga	acgcagtggg	360
gacaaggacc	tgccctcatt	ggctgtgggc	atatgtgagg	agcatggatc	cgccatggcc	420
ccccagcaca	tcctggcctc	tgggtcaact	gctggcccca	agctgtaccc	caagctatac	480
acagatgtgc	acacacacac	acatacacac	acctgcactc	acacgctctc	atgtggaggg	540
caaggttcat	caacaccagc	atgtccacta	tcagtgtctaa	atacagcgaa	tctccaagca	600
ctgtgtcctg	aggtaggcat	ttggggggcca	aggcaacagg	ttggggagaat	tgagaacaat	660
ggaggaagag	tatcttag					678

<210> 105
 <211> 225
 <212> PRT
 <213> Mouse

<400> 105

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
			20					25					30		
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln
			35				40					45			
Trp	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser
	50					55				60					
Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val
65					70				75						80
Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys
				85				90					95		
Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro
			100					105					110		
Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala
			115				120					125			
Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile
	130					135					140				
Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr
145					150				155						160
Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu
				165				170						175	
Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val
			180					185					190		
Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp
		195				200					205				
Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val
	210					215					220				
Ser															
225															

<210> 106
 <211> 882
 <212> DNA
 <213> Mouse

<400> 106

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cctgtgggta	gctctgtgcg	gctcaagtgt	gtggccagtg	ggcaccacg	gccagacatc	180
atgtggatga	aggatgacca	gaccttgacg	catctagagg	ctagtgaaca	cagaaagaag	240
aagtggacac	tgagcttgaa	gaacctgaag	cctgaagaca	gtggcaagta	cacgtgccgt	300
gtatctaaca	aggccggtgc	catcaacgcc	acctacaaag	tggatgtaat	ccaccccaaa	360
cctccagggc	ctcctatggc	ttcttcatcg	tcatccacaa	gcctgccatg	gcctgtggtg	420
atcggcatcc	cagctggtgc	tgtcttcatc	ctaggcactg	tgctgctctg	gctttgccag	480
accaagaaga	agccatgtgc	cccagcatct	acacttcctg	tgccctgggca	tcgtcccca	540
gggacatccc	gagaacgcag	tggtgacaag	gacctgccct	cattggctgt	gggcatatgt	600
gaggagcatg	gatccgccat	ggccccccag	cacatcctgg	cctctggctc	aactgctggc	660
cccaagctgt	acccaagct	atacacagat	gtgcacacac	acacacatac	acacacctgc	720
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ctaaatacag	cgaatctcca	agcactgtgt	cctgaggtag	gcatttgggg	gccaaggcaa	840
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<210> 107

<211> 293

<212> PRT

<213> Mouse

<400> 107

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1				5				10					15		
Ser	Ala	Glu	Ala	Ala	Arg	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys
			20					25					30		
Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu
		35					40					45			
Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys
	50					55					60				
Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys
65					70				75					80	
Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys
			85					90						95	
Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr
			100					105					110		
Lys	Val	Asp	Val	Ile	His	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser
		115					120					125			
Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro
		130				135					140				
Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln
145					150					155					160
Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly
				165				170						175	
His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu
		180						185					190		
Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala
		195					200					205			
Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr
		210				215					220				
Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr	Cys
225					230					235					240
Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys
			245					250						255	
Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu
			260					265					270		
Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn
		275					280					285			
Gly	Gly	Arg	Val	Ser											

290

<210> 108
<211> 951
<212> DNA
<213> Mouse

<400> 108
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gtggacttcg gtgggacaac gtccttccag tgcaagggtg gcagtgcgt gaagcctgtg 180
atccagtggc tgaagcgggt ggagtacggc tccgaggggac gccacaactc caccattgat 240
gtgggtggcc agaagtttgt ggtgttgccc acgggtgatg tgtggtcacg gcctgatggc 300
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gaccccaaac ctccagggcc tcctatggct tcttcatcgt catccacaag cctgccatgg 480
cctgtggtga tcggcatccc agctggtgct gtcttcatcc taggcactgt gctgctctgg 540
ctttgccaga ccaagaagaa gccatgtgcc ccagcatcta cacttcctgt gcctgggcat 600
cgtcccccag ggacatcccc agaacgcagt ggtgacaagg acctgccctc attggctgtg 660
ggcatatgtg aggagcatgg atccgccatg gccccccagc acatcctggc ctctggctca 720
actgctggcc ccaagctgta cccaagcta tacacagatg tgcacacaca cacacataca 780
cacacctgca ctcacacgct ctcatgtgga gggcaagggt catcaacacc agcatgtcca 840
ctatcagtgc taaatacagc gaatctccaa gcactgtgtc ctgaggtagg catttggggg 900
ccaaggcaac aggttgggag aattgagaac aatggaggaa gagtatctta g 951

<210> 109
<211> 316
<212> PRT
<213> Mouse

<400> 109
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
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20 25 30
Gly Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser
35 40 45
Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu
50 55 60
Lys Arg Val Glu Tyr Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp
65 70 75 80
Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser
85 90 95
Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg
100 105 110
Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly
115 120 125
Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro Asp Pro Lys Pro
130 135 140
Pro Gly Pro Pro Met Ala Ser Ser Ser Ser Ser Thr Ser Leu Pro Trp
145 150 155 160
Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr
165 170 175
Val Leu Leu Trp Leu Cys Gln Thr Lys Lys Lys Pro Cys Ala Pro Ala
180 185 190
Ser Thr Leu Pro Val Pro Gly His Arg Pro Pro Gly Thr Ser Arg Glu

	195		200		205
Arg	Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Val Gly Ile Cys Glu				
	210		215		220
Glu	His Gly Ser Ala Met Ala Pro Gln His Ile Leu Ala Ser Gly Ser				
225		230		235	240
Thr	Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Val His Thr				
	245		250		255
His	Thr His Thr His Thr Cys Thr His Thr Leu Ser Cys Gly Gly Gln				
	260		265		270
Gly	Ser Ser Thr Pro Ala Cys Pro Leu Ser Val Leu Asn Thr Ala Asn				
	275		280		285
Leu	Gln Ala Leu Cys Pro Glu Val Gly Ile Trp Gly Pro Arg Gln Gln				
	290		295		300
Val	Gly Arg Ile Glu Asn Asn Gly Gly Arg Val Ser				
305		310		315	

<210> 110
 <211> 597
 <212> DNA
 <213> Mouse

<400> 110

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ccatggcctg	tggtgatcgg	catcccagct	ggtgctgtct	tcatcctagg	cactgtgctg	180
ctctggcttt	gccagaccaa	gaagaagcca	tgtgccccag	catctacact	tcctgtgcct	240
gggcatcgtc	ccccaggac	atcccagagaa	cgcagtgggtg	acaaggacct	gccctcattg	300
gctgtgggca	tatgtgagga	gcatggatcc	gccatggccc	cccagcacat	cctggcctct	360
ggctcaactg	ctggcccca	gctgtacccc	aagctataca	cagatgtgca	cacacacaca	420
catacacaca	cctgcactca	cacgctctca	tgtggagggc	aagggttcac	aacaccagca	480
tgtccactat	cagtgtctaaa	tacagcgaat	ctccaagcac	tgtgtcctga	ggtaggcatt	540
tggggggcaa	ggcaacaggt	tgggagaatt	gagaacaatg	gaggaagagt	atcttag	597

<210> 111
 <211> 198
 <212> PRT

<213> Mouse

<400> 111

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Ala	Arg	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala
			20					25					30		
Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile
		35					40					45			
Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys
	50					55					60				
Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro
65					70				75						80
Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp
			85					90					95		
Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met
		100						105					110		
Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu
		115					120					125			
Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr

130		135		140
Cys Thr His Thr Leu Ser	Cys Gly Gly Gln Gly	Ser Ser Thr Pro Ala		
145	150	155	160	
Cys Pro Leu Ser Val Leu	Asn Thr Ala Asn Leu	Gln Ala Leu Cys Pro		
	165	170	175	
Glu Val Gly Ile Trp Gly	Pro Arg Gln Gln Val	Gly Arg Ile Glu Asn		
	180	185	190	
Asn Gly Gly Arg Val Ser				
195				

<210> 112
 <211> 1060
 <212> DNA
 <213> Mouse

<400> 112

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cgcactgtgc	ggctacagt	cccagtgagg	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccaggggtctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccaggggaag	360
gagagccctg	ggccagggtg	ttcttcgggg	ggccaggagg	accagccag	ccagcagtgg	420
gcacggcctc	gcttcacaca	gccctccaag	atgaggcgcc	gagtgattgc	acggcctgtg	480
ggtagctctg	tgcggctcaa	gtgtgtggcc	agtgggcacc	cacggccaga	catcatgtgg	540
atgaaggatg	accagacctt	gacgcattct	gaggctagtg	aacacagaaa	gaagaagtgg	600
acactgagct	tgaagaacct	gaagcctgaa	gacagtggca	agtacacgtg	ccgtgtatct	660
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aagcctgtgc	tcacagggac	acaccctgtg	aacacaacgg	tggacttcgg	tgggacaacg	780
tccttccagt	gcaaggtgcg	cagtgcctgt	aagcctgtga	tccagtggct	gaagcgggtg	840
gagtacggct	ccgaggggac	ccacaactcc	accattgatg	tgggtggcca	gaagtttgtg	900
gtgttgccca	cgggtgatgt	gtgggtcacg	cctgatggct	cctacctcaa	caagctgctc	960
atctctcggg	cccgccagga	tgatgctggc	atgtacatct	gcctaggtgc	aaataccatg	1020
ggctacagtt	tccgtagcgc	cttcctcact	gtattaccag			1060

<210> 113
 <211> 353
 <212> PRT
 <213> Mouse

<400> 113

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro	
1 5 10 15	
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val	
20 25 30	
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro	
35 40 45	
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg	
50 55 60	
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu	
65 70 75 80	
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys	
85 90 95	
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile	
100 105 110	
Met Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly Pro Gly Gly Ser	
115 120 125	

Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg
130						135					140				
Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val
145					150					155					160
Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro
				165					170					175	
Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala
			180					185					190		
Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys
		195					200					205			
Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly
		210				215					220				
Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser
225					230					235					240
Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe
				245					250					255	
Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro
			260					265					270		
Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg	His
		275					280					285			
Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr
		290				295					300				
Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu
305					310					315					320
Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly
				325					330					335	
Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu
			340					345					350		

Pro

<210> 114
 <211> 706
 <212> DNA
 <213> Mouse

<400> 114

atgacgcgga	gccccgcgct	gctgctgctg	ctattggggg	ccctcccgtc	ggctgaggcg	60
gcgcgaggac	ccccagaat	ggcagacaaa	gtggtccac	ggcaggtggc	ccgcctgggc	120
cgcactgtgc	ggctacagt	cccagtggag	ggggaccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggctctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccaggggaag	360
gagagccctg	ggccagggtg	ttcttcgggg	ggccaggagg	accagccag	ccagcagtgg	420
gcacggcctc	gcttcacaca	gccctccaag	atgaggcgcc	gagtgattgc	acggcctgtg	480
ggtagctctg	tgcggctcaa	gtgtgtggcc	agtgggcacc	cacggccaga	catcatgtgg	540
atgaaggatg	accagacctt	gacgcactta	gaggctagt	aacacagaaa	gaagaagtgg	600
acactgagct	tgaagaacct	gaagcctgaa	gacagtggca	agtacacgtg	ccgtgtatct	660
aacaaggccg	gtgccatcaa	cgccacctac	aaagtggatg	taatcc		706

<210> 115
 <211> 235
 <212> PRT
 <213> Mouse

<400> 115

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro

1				5					10					15			
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val		
			20					25					30				
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro		
		35					40					45					
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg		
	50					55					60						
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu		
65					70				75						80		
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys		
			85					90					95				
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile		
		100					105					110					
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly	Ser		
		115				120					125						
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg		
	130					135					140						
Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val		
145					150					155					160		
Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro		
			165					170					175				
Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala		
		180				185						190					
Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys		
	195					200					205						
Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly		
	210				215						220						
Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile							
225				230				235									

<210> 116
 <211> 775
 <212> DNA
 <213> Mouse

<400> 116	
atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg	60
gcgcgaggac cccaagaat ggcagacaaa gtgggtccac ggcaggtggc ccgcctgggc	120
cgcactgtgc ggctacagtg cccagtggag ggggaccac caccgttgac catgtggacc	180
aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggtctg	240
aaggtgaagg aggtggaggc cgaggatgcc ggtgtttatg tgtgcaaggc caccaatggc	300
tttggcagcc tcagcgtcaa ctacactctc atcatcatgg atgatattag tccagggaag	360
gagagccctg ggccagggtg ttcttcgggg ggccaggagg acccagccag ccagcagtgg	420
gagcggactc gttccaagcc tgtgctcaca gggacacacc ctgtgaacac aacgggtggc	480
ttcgggtggga caacgtcctt ccagtgcagg gtgcgcagtg acgtgaagcc tgtgatccag	540
tggctgaagc ggggtggagta cggctccgag ggacgccaca actccaccat tgatgtgggt	600
ggccagaagt ttgtggtgtt gccacgggt gatgtgtggt cacggcctga tggctcctac	660
ctcaacaagc tgctcatctc tcgggcccgc caggatgatg ctggcatgta catctgccta	720
ggtgcaaata ccatgggcta cagtttccgt agcgccttcc tctactgtatt accag	775

<210> 117
 <211> 258
 <212> PRT
 <213> Mouse

<400> 117

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1				5				10						15	
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
			20					25					30		
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
		35					40					45			
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
	50					55					60				
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
65					70				75						80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
			85					90					95		
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
		100						105					110		
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly	Ser
		115					120					125			
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Glu	Arg	Thr	Arg
	130					135					140				
Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp
145					150					155					160
Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys
			165					170					175		
Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg
		180					185						190		
His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro
	195						200					205			
Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu
	210				215						220				
Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu
225					230				235						240
Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val
			245					250					255		

Leu Pro

<210> 118
 <211> 979
 <212> DNA
 <213> Mouse

<400> 118

atgacgcgga	gccccgcgct	gctgctgctg	ctattggggg	ccctcccgtc	ggctgaggcg	60
gcgcgaggac	ccccagaat	ggcagacaaa	gtgggtccac	ggcaggtggc	ccgcctgggc	120
cgcactgtgc	ggctacagt	cccagtggag	ggggaccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggctctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	cacggcctcg	cttcacacag	360
ccctccaaga	tgaggcgccg	agtgattgca	cggcctgtgg	gtagctctgt	gcggtcaag	420
tgtgtggcca	gtgggcaccc	acggccagac	atcatgtgga	tgaaggatga	ccagaccttg	480
acgcatctag	aggctagtga	acacagaaag	aagaagtgga	cactgagctt	gaagaacctg	540
aagcctgaag	acagtggcaa	gtacacgtgc	cgtgtatcta	acaaggccgg	tgccatcaac	600
gccacctaca	aagtggatgt	aatccagcgg	actcgttcca	agcctgtgct	cacagggaca	660
caccctgtga	acacaacggt	ggacttcggt	gggacaacgt	ccttccagt	caaggtgcgc	720
agtgacgtga	agcctgtgat	ccagtggctg	aagcgggtgg	agtacggctc	cgagggacgc	780
cacaactcca	ccattgatgt	gggtggccag	aagtttgtgg	tgttgccac	gggtgatgtg	840
tggtcacggc	ctgatggctc	ctacctcaac	aagctgctca	tctctcgggc	ccgccaggat	900

gatgctggca tgtacatctg cctaggtgca aataccatgg gctacagttt ccgtagcgcc
 ttccctcactg tattaccag

960
 979

<210> 119
 <211> 326
 <212> PRT
 <213> Mouse

<400> 119
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
 20 25 30
 Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
 35 40 45
 Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
 50 55 60
 Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
 65 70 75 80
 Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
 85 90 95
 Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
 100 105 110
 Met Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val
 115 120 125
 Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser
 130 135 140
 Gly His Pro Arg Pro Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu
 145 150 155 160
 Thr His Leu Glu Ala Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser
 165 170 175
 Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val
 180 185 190
 Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile
 195 200 205
 Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn
 210 215 220
 Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg
 225 230 235 240
 Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly
 245 250 255
 Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe
 260 265 270
 Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr
 275 280 285
 Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met
 290 295 300
 Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala
 305 310 315 320
 Phe Leu Thr Val Leu Pro
 325

<210> 120
 <211> 787
 <212> DNA
 <213> Mouse

<400> 120

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atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg      60
gcgcgagatg atattagtcc agggaaggag agccctgggc caggtgggtc ttcggggggc      120
caggaggacc cagccagcca gcagtgggca cggcctcgct tcacacagcc ctccaagatg      180
aggcgccgag tgattgcacg gcctgtgggt agctctgtgc ggctcaagtg tgtggccagt      240
gggcacccac ggccagacat catgtggatg aaggatgacc agaccttgac gcatctagag      300
gctagtgaac acagaaagaa gaagtggaca ctgagcttga agaacctgaa gcctgaagac      360
agtggcaagt acacgtgccg tgtatctaac aaggccggtg ccatcaacgc cacctacaaa      420
gtggatgtaa tccagcggac tcgttccaag cctgtgctca cagggaacaca ccctgtgaac      480
acaacggtgg acttcggtgg gacaacgtcc ttccagtgcag aggtgcgcag tgacgtgaag      540
cctgtgatcc agtggctgaa gcgggtggag tacggctccg agggacgcca caactccacc      600
attgatgtgg gtggccagaa gtttgtggtg ttgccacggg gtgatgtgtg gtcacggcct      660
gatggctcct acctcaacaa gctgctcatc tctcggggcc gccaggatga tgctggcatg      720
tacatctgcc taggtgcaaa taccatgggc tacagtttcc gtagcgcctt cctcactgta      780
ttaccag                                         787
```

<210> 121

<211> 262

<212> PRT

<213> Mouse

<400> 121

```
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1          5          10          15
Ser Ala Glu Ala Ala Arg Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro
          20          25          30
Gly Pro Gly Gly Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln
          35          40          45
Trp Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val
          50          55          60
Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser
65          70          75          80
Gly His Pro Arg Pro Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu
          85          90          95
Thr His Leu Glu Ala Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser
          100          105          110
Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val
          115          120          125
Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile
          130          135          140
Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn
          145          150          155          160
Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg
          165          170          175
Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly
          180          185          190
Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe
          195          200          205
Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr
          210          215          220
Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met
          225          230          235          240
Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala
          245          250          255
Phe Leu Thr Val Leu Pro
          260
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<210> 122
 <211> 421
 <212> DNA
 <213> Mouse

<400> 122
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 gcgcgaggac ccccaagaat ggcagacaaa gtggtccac ggcaggtggc ccgcctgggc 120
 cgcactgtgc ggctacagtg cccagtggag ggggaccac caccgttgac catgtggacc 180
 aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggtctg 240
 aaggtgaagg aggtggaggc cgaggatgcc ggtgtttatg tgtgcaaggc caccaatggc 300
 tttggcagcc tcagcgtcaa ctacactctc atcatcatgg atgatattag tccagggaag 360
 gagagccctg ggccaggtgg ttcttcgggg ggccaggagg acccagccag ccagcagtgg 420
 g 421

<210> 123
 <211> 140
 <212> PRT
 <213> Mouse

<400> 123
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
 20 25 30
 Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
 35 40 45
 Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
 50 55 60
 Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
 65 70 75 80
 Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
 85 90 95
 Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
 100 105 110
 Met Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly Pro Gly Gly Ser
 115 120 125
 Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp
 130 135 140

<210> 124
 <211> 625
 <212> DNA
 <213> Mouse

<400> 124
 atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
 gcgcgaggac ccccaagaat ggcagacaaa gtggtccac ggcaggtggc ccgcctgggc 120
 cgcactgtgc ggctacagtg cccagtggag ggggaccac caccgttgac catgtggacc 180
 aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggtctg 240
 aaggtgaagg aggtggaggc cgaggatgcc ggtgtttatg tgtgcaaggc caccaatggc 300
 tttggcagcc tcagcgtcaa ctacactctc atcatcatgg cagggcctcg cttcacacag 360
 ccctccaaga tgaggcgccg agtgattgca cggcctgtgg gtagctctgt gcggctcaag 420
 tgtgtggcca gtgggcaccc acggccagac atcatgtgga tgaaggatga ccagacctg 480
 acgcatctag aggctagtga acacagaaag aagaagtgga cactgagctt gaagaacctg 540
 aagcctgaag acagtggcaa gtacacgtgc cgtgtatcta acaaggccgg tgccatcaac 600

gccacctaca aagtggatgt aatcc

625

<210> 125
<211> 208
<212> PRT
<213> Mouse

<400> 125
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
1 5 10 15
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
20 25 30
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
35 40 45
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
50 55 60
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
65 70 75 80
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
85 90 95
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
100 105 110
Met Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val
115 120 125
Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser
130 135 140
Gly His Pro Arg Pro Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu
145 150 155 160
Thr His Leu Glu Ala Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser
165 170 175
Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val
180 185 190
Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile
195 200 205

<210> 126
<211> 694
<212> DNA
<213> Mouse

<400> 126
atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
gcgcgaggac ccccaagaat ggcagacaaa gtggtccac gccaggtggc ccgcctgggc 120
cgactgtgc ggctacagt cccagtggag ggggacccac caccgttgac catgtggacc 180
aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggtctg 240
aaggtgaagg aggtggaggc cgaggatgcc ggtgtttatg tgtgcaaggc caccaatggc 300
tttggcagcc tcagcgtcaa ctacactctc atcatcatgg agcggactcg ttccaagcct 360
gtgctcacag ggacacaccc tgtgaacaca acggtggact tcggtgggac aacgtccttc 420
cagtgaagg tgcgcagtga cgtgaagcct gtgatccagt ggctgaagcg ggtggagtac 480
ggctccgagg gacgccacaa ctccaccatt gatgtgggtg gccagaagtt tgtgggtgtg 540
cccacgggtg atgtgtggtc acggcctgat ggctcctacc tcaacaagct gctcatctct 600
cgggcccgcc aggatgatgc tggcatgtac atctgcctag gtgcaaatac catgggctac 660
agtttccgta gcgccttct cactgtatta ccag 694

<210> 127
<211> 231
<212> PRT

<213> Mouse

<400> 127

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Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1          5          10          15
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
          20          25          30
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
          35          40          45
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
 50          55          60
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
65          70          75          80
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
          85          90          95
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
          100          105          110
Met Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val
          115          120          125
Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val
          130          135          140
Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr
          145          150          155          160
Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys
          165          170          175
Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser
          180          185          190
Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly
          195          200          205
Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser
          210          215          220
Ala Phe Leu Thr Val Leu Pro
225          230
```

<210> 128

<211> 433

<212> DNA

<213> Mouse

<400> 128

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gcgcgagatg atattagtcc agggaaggag agccctgggc caggtgggtc ttcggggggc      120
caggaggacc cagccagcca gcagtgggca cggcctcgct tcacacagcc ctccaagatg      180
aggcgccgag tgattgcacg gcctgtgggt agctctgtgc ggctcaagtg tgtggccagt      240
gggcacccac ggccagacat catgtggatg aaggatgacc agaccttgac gcatctagag      300
gctagtgaac acagaaagaa gaagtggaca ctgagcttga agaacctgaa gcctgaagac      360
agtggcaagt acacgtgccg tgtatctaac aaggccggtg ccatcaacgc cacctacaaa      420
gtggatgtaa tcc                                     433
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<210> 129

<211> 144

<212> PRT

<213> Mouse

<400> 129

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Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1          5          10          15
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Ser	Ala	Glu	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
			20					25					30		
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln
		35					40					45			
Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val
	50					55					60				
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser
65					70					75					80
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu
				85					90					95	
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser
			100					105					110		
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val
		115					120					125			
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile
	130					135					140				

<210> 130
 <211> 502
 <212> DNA
 <213> Mouse

<400> 130	
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gcgcgagatg atattagtcc aggggaaggag agccctgggc caggtgggtc ttcggggggc	120
caggaggacc cagccagcca gcagtgggag cggactcggt ccaagcctgt gctcacaggg	180
acacaccctg tgaacacaac ggtggacttc ggtgggacaa cgtccttcca gtgcaagggtg	240
cgcagtgacg tgaagcctgt gatccagtgg ctgaagcggg tggagtacgg ctccgaggga	300
cgccacaact ccaccattga tgtgggtggc cagaagtttg tgggtgttgcc cacgggtgat	360
gtgtgggtcac ggccctgatgg ctccctacctc aacaagctgc tcatctctcg ggcccgccag	420
gatgatgctg gcatgtacat ctgcctaggt gcaaatacca tgggctacag tttccgtagc	480
gccttcctca ctgtattacc ag	502

<210> 131
 <211> 167
 <212> PRT
 <213> Mouse

<400> 131	
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro	
1	15
Ser Ala Glu Ala Ala Arg Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro	
	30
Gly Pro Gly Gly Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln	
	45
Trp Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val	
50	60
Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val	
65	80
Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr	
	95
Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys	
	110
Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser	
	125
Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly	
130	140

Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser
 145 150 155 160
 Ala Phe Leu Thr Val Leu Pro
 165

<210> 132
 <211> 706
 <212> DNA
 <213> Mouse

<400> 132
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 cctgtgggta gctctgtgcg gctcaagtgt gtggccagtg ggcacccacg gccagacatc 180
 atgtggatga aggatgacca gaccttgacg catctagagg ctagtgaaca cagaaagaag 240
 aagtggacac tgagcttgaa gaacctgaag cctgaagaca gtggcaagta cacgtgccgt 300
 gtatctaaca aggccggtgc catcaacgcc acctacaaag tggatgtaat ccagcggact 360
 cgttccaagc ctgtgctcac agggacacac cctgtgaaca caacggtgga cttcggtggg 420
 acaacgtcct tccagtgcaa ggtgcgcagt gacgtgaagc ctgtgatcca gtggctgaag 480

 cgggtggagt acggctccga gggacgccac aactccacca ttgatgtggg tggccagaag 540
 tttgtggtgt tgccacggg tgatgtgtgg tcacggcctg atggctccta cctcaacaag 600
 ctgctcatct ctcgggcccg ccaggatgat gctggcatgt acatctgcct aggtgcaaat 660
 accatgggct acagtttccg tagcgccttc ctcactgtat taccag 706

<210> 133
 <211> 235
 <212> PRT
 <213> Mouse

<400> 133
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys
 20 25 30
 Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu
 35 40 45
 Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Met Trp Met Lys
 50 55 60
 Asp Asp Gln Thr Leu Thr His Leu Glu Ala Ser Glu His Arg Lys Lys
 65 70 75 80
 Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys
 85 90 95
 Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr
 100 105 110
 Lys Val Asp Val Ile Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly
 115 120 125
 Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe
 130 135 140
 Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys
 145 150 155 160
 Arg Val Glu Tyr Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val
 165 170 175
 Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg
 180 185 190
 Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln
 195 200 205

Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr
 210 215 220
 Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro
 225 230 235

<210> 134
 <211> 340
 <212> DNA
 <213> Mouse

<400> 134
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 gcgcgaggac cccaagaat ggcagacaaa gtgggtccac ggcagggtggc ccgcctgggc 120
 cgcactgtgc ggctacagtg cccagtggag ggggaccac caccgttgac catgtggacc 180
 aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggtctg 240
 aagggtgaagg aggtggaggc cgaggatgcc ggtgtttatg tgtgcaaggc caccaatggc 300
 tttggcagcc tcagcgtcaa ctacactctc atcatcatgg 340

<210> 135
 <211> 113
 <212> PRT
 <213> Mouse

<400> 135
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
 20 25 30
 Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
 35 40 45
 Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
 50 55 60
 Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
 65 70 75 80
 Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
 85 90 95
 Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
 100 105 110
 Met

<210> 136
 <211> 148
 <212> DNA
 <213> Mouse

<400> 136
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 gcgcgagatg atattagtcc agggaaggag agccctgggc cagggtggttc ttcggggggc 120
 caggaggacc cagccagcca gcagtggg 148

<210> 137
 <211> 49
 <212> PRT
 <213> Mouse

<400> 137

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro
 20 25 30
 Gly Pro Gly Gly Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln
 35 40 45
 Trp

<210> 138
 <211> 352
 <212> DNA
 <213> Mouse

<400> 138
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 gcgcgagcac ggctcgtt cacacagccc tccaagatga ggcgccgagt gattgcacgg 120
 cctgtgggta gctctgtgcg gctcaagtgt gtggccagtg ggcacccacg gccagacatc 180
 atgtggatga aggatgacca gaccttgacg catctagagg ctagtgaaca cagaaagaag 240
 aagtggacac tgagcttgaa gaacctgaag cctgaagaca gtggcaagta cacgtgccgt 300
 gtatctaaca aggccggtgc catcaacgcc acctacaaag tggatgtaat cc 352

<210> 139
 <211> 117
 <212> PRT
 <213> Mouse

<400> 139

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys
 20 25 30
 Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu
 35 40 45
 Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Met Trp Met Lys
 50 55 60
 Asp Asp Gln Thr Leu Thr His Leu Glu Ala Ser Glu His Arg Lys Lys
 65 70 75 80
 Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys
 85 90 95
 Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr
 100 105 110
 Lys Val Asp Val Ile
 115

<210> 140
 <211> 421
 <212> DNA
 <213> Mouse

<400> 140
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 gcgcgagagc ggactcgttc caagcctgtg ctcacaggga cacaccctgt gaacacaacg 120
 gtggacttcg gtgggacaac gtccttccag tgcaaggtgc gcagtacgt gaagcctgtg 180
 atccagtggc tgaagcgggt ggagtacggc tccgaggac gccacaactc caccattgat 240
 gtgggtggcc agaagtttgt ggtgttgccc acgggtgatg tgtggtcacg gcctgatggc 300

tcctacctca acaagctgct catctctcgg gcccgccagg atgatgctgg catgtacatc	360
tgccntaggtg caaataccat gggctacagt ttccgtagcg ccttcctcac tgtattacca	420
g	421

<210> 141
 <211> 140
 <212> PRT
 <213> Mouse

<400> 141
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Glu Arg Thr Arg Ser Lys Pro Val Leu Thr
 20 25 30
 Gly Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser
 35 40 45
 Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu
 50 55 60
 Lys Arg Val Glu Tyr Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp
 65 70 75 80
 Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser
 85 90 95
 Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg
 100 105 110
 Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly
 115 120 125
 Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro
 130 135 140

<210> 142
 <211> 67
 <212> DNA
 <213> Mouse

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gcgcgag	67

<210> 143
 <211> 22
 <212> PRT
 <213> Mouse

<400> 143
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg
 20

<210> 144
 <211> 1389
 <212> DNA
 <213> Mouse

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gcgcgaggac cccaagaat ggcagacaaa gtgggtccac ggcaggtggc ccgcctgggc	120

cgcaactgtgc	ggctacagt	cccagtgag	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccaggggtctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatgtgga	tgaaggatga	ccagaccttg	360
acgcatctag	aggctagtga	acacagaaaag	aagaagtgga	cactgagctt	gaagaacctg	420
aagcctgaag	acagtggcaa	gtacacgtgc	cgtgtatcta	acaaggccgg	tgccatcaac	480
gccacctaca	aagtggatgt	aatccagcgg	actcgttcca	agcctgtgct	cacagggaca	540
caccctgtga	acacaacggc	ggacttcggt	gggacaacgt	ccttccagtg	caaggtgcgc	600
agtgacgtga	agcctgtgat	ccagtggctg	aagcgggtgg	agtacggctc	cgagggacgc	660
cacaactcca	ccattgatgt	gggtggccag	aagtgttggt	tgttgcccac	gggtgatgtg	720
tggtcacggc	ctgatggctc	ctacctcaac	aagctgctca	tctctcgggc	ccgccaggat	780
gatgctggca	tgtacacctg	cctaggtgca	aataccatgg	gctacagttt	ccgtagcgcc	840
ttcctcactg	tattaccaga	cccaaacct	ccagggcctc	ctatggcttc	ttcatcgtea	900
tccacaagcc	tgccatggcc	tgtggtgatc	ggcatcccag	ctggtgctgt	cttcatccta	960
ggcactgtgc	tgctctggct	ttgccagacc	aagaagaagc	catgtgcccc	agcatctaca	1020
cttcctgtgc	ctgggcatcg	tccccaggg	acatcccag	aacgcagtgg	tgacaaggac	1080
ctgccctcat	tggctgtggg	catatgtgag	gagcatggat	ccgccatggc	cccccagcac	1140
atcctggcct	ctggctcaac	tgctggcccc	aagctgtacc	ccaagctata	cacagatgtg	1200
cacacacaca	cacatacaca	cacctgcact	cacacgctct	catgtggagg	gcaaggttca	1260
tcaacaccag	catgtccact	atcagtgcta	aatacagcga	atctccaagc	actgtgtcct	1320
gaggtaggca	tatggggggc	aaggcaacag	gttggggagaa	ttgagaacaa	tggaggaaga	1380
gtatcttag						1389

<210> 145

<211> 462

<212> PRT

<213> Mouse

<400> 145

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val
			20					25					30	Val
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys
		35					40					45		Pro
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly
	50					55					60			Arg
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly
65					70				75					80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys
			85					90					95	Lys
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile
			100					105					110	Met
Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala	Ser	Glu
		115					120					125		His
Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys	Pro	Glu
	130					135					140			Asp
Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly	Ala	Ile
145					150				155					160
Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro
			165					170					175	Val
Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly
		180						185					190	Thr
Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile
		195					200					205		Gln
Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg	His	Asn	Ser
	210					215					220			Thr

Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	225	230	235	240
Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	245	250	255	
Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	260	265	270	
Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	275	280	285	
Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	290	295	300	
Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	305	310	315	320
Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	325	330	335	
Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	340	345	350	
Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	355	360	365	
Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	370	375	380	
Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	385	390	395	400
His	Thr	His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu	Ser	Cys	Gly	405	410	415	
Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr	420	425	430	
Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg	435	440	445	
Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val	Ser			450	455	460	